GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 23, 2006, 16:44:52 ; Search time 38 Seconds
(without alignments)
45.576 Million cell updates/sec

Title: US-09-830-972A-2_COPY_623_640
Perfect score: 99
Sequence: 1 SYDSIKLEPENPPPYEEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	51.5	2957	2	T33152	hypothetical prote
2	50	50.5	442	2	S58738	nitrate-binding pr
3	50	50.5	473	2	A56377	rubber particle cy
4	49	49.5	458	2	AF2165	bicarbonate transp
5	49	49.5	1398	2	T25568	hypothetical prote
6	48.5	49.0	307	2	T40240	dimethylase - fiss
7	48.5	49.0	315	2	T43249	rRNA (adenine-N6,N
8	48	48.5	90	1	ZNXPLC	zinc finger protei
9	47	47.5	257	2	F75084	hypothetical prote
10	47	47.5	591	2	T51996	hypothetical prote
11	47	47.5	591	2	T41531	activator of Hsp70
12	46	46.5	141	2	PC4290	peroxisome prolife
13	46	46.5	156	2	T18755	hypothetical prote
14	46	46.5	156	2	F89418	protein B0413.7 [i
15	46	46.5	330	2	G83853	spore cortex-lytic
16	46	46.5	340	2	T49887	hypothetical prote
17	46	46.5	475	2	JC4264	peroxisome prolife
18	46	46.5	505	2	JC4859	peroxisome prolife
19	46	46.5	505	2	A54101	peroxisome prolife
20	46	46.5	539	2	T21816	hypothetical prote
21	46	46.5	1113	2	T20140	hypothetical prote
22	45	45.5	317	2	T00986	yeast pheromone re
23	45	45.5	400	2	T29121	hypothetical prote
24	45	45.5	459	2	G83784	glycerol-3-phospha
25	45	45.5	465	2	A44498	radial spoke prote
26	45	45.5	475	2	JE0279	peroxisome prolife
27	45	45.5	477	2	C42214	peroxisome prolife
28	45	45.5	487	2	JC2495	histamine H1 recep
29	45	45.5	504	2	JE0280	peroxisome prolife
30	45	45.5	505	2	JC5777	peroxisome prolife
31	44.5	44.9	211	2	C82748	stringent starvati
32	44	44.4	194	2	T22209	hypothetical prote
33	44	44.4	250	2	S36769	ubiquitin-protein
34	44	44.4	413	2	T02463	hypothetical prote
35	44	44.4	423	2	A30819	interferon-regulat
36	44	44.4	446	2	S77389	nitrate transport
37	44	44.4	483	2	T24856	hypothetical prote
38	44	44.4	520	2	G88846	protein T12A7.2 [i
39	44	44.4	613	2	T00853	hypothetical prote
40	44	44.4	631	2	A31203	interferon-regulat
41	44	44.4	661	2	T15073	hypothetical prote
42	44	44.4	754	2	A56619	female sterile hom
43	44	44.4	2434	2	S44861	DNA topoisomerase
44	44	44.4	3951	1	VFIHB1	F1 protein - avian
45	43.5	43.9	174	2	F75097	adenylylsulfate 3-

ALIGNMENTS

RESULT 1
T33152
hypothetical protein T04D1.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33152
R;Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid T04D1.
A;Reference number: Z21292
A;Accession: T33152
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2957 <DAV>
A;Cross-references: UNIPROT:O61845; UNIPARC:UPI000007A573; EMBL:AF067617; PIDN:AAC17559.1
A;Experimental source: strain Bristol N2; clone T04D1
C;Genetics:
A;Gene: CESP:T04D1.4
A;Map position: 1
A;Introns: 122/3; 293/3; 515/3; 1205/2; 1577/1; 2221/3; 2776/1; 2864/3

Query Match 51.5%; Score 51; DB 2; Length 2957;
Best Local Similarity 53.8%; Pred. No. 64;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 IKLEPENPPPYEE 17
              :|:||| | ||::
Db        464 VKMEPEKPSPYQQ 476
```

RESULT 2
S58738
nitrate-binding protein nrtA precursor, periplasmic [similarity] - Phormidium laminosum
C;Species: Phormidium laminosum
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S58738; S56641; S62124
R;Merchan, F.; Kindle, K.L.; Llama, M.J.; Serra, J.L.; Fernandez, E.
Plant Mol. Biol. 28, 759-766, 1995
A;Title: Cloning and sequencing of the nitrate transport system from the thermophilic, fi
cus sp. PCC 7942.
A;Reference number: S58738; MUID:95375238; PMID:7647306
A;Accession: S58738
A;Molecule type: DNA
A;Residues: 1-442 <MER>
A;Cross-references: UNIPROT:Q51880; UNIPARC:UPI00000B7E94; EMBL:Z19598; NID:g1154890; PII
R;Merchan, F.; Prieto, R.; Kindle, K.L.; Llama, M.J.; Serra, J.L.; Fernandez, E.
Plant Mol. Biol. 27, 1037-1042, 1995
A;Title: Isolation, sequence and expression in Escherichia coli of the nitrite reductase
A;Reference number: S56640; MUID:95284340; PMID:7766873
A;Accession: S56641
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

```
A;Residues: 1-67,'A',69-442 <MEW>
A;Cross-references: UNIPARC:UPI000017CAF6; EMBL:Z19598
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics:
A;Gene: nrtA
C;Keywords: nitrate transport; periplasmic space

  Query Match             50.5%;  Score 50;  DB 2;  Length 442;
  Best Local Similarity   47.1%;  Pred. No. 10;
  Matches    8;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 YDSIKLEPENPPPYEEA 18
              :| :| :||||  |  |
Db        420 FDGVKFDPENPSAYLSA 436


RESULT 3
A56377
rubber particle cytochrome P450 - guayule
C;Species: Parthenium argentatum (guayule)
C;Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A56377
R;Pan, Z.; Durst, F.; Werck-Reichhart, D.; Gardner, H.W.; Camara, B.; Cornish, K.; Backh
J. Biol. Chem. 270, 8487-8494, 1995
A;Title: The major protein of guayule rubber particles is a cytochrome P450. Characteriz
A;Reference number: A56377; MUID:95238331; PMID:7721745
A;Accession: A56377
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-473 <PAN>
A;Cross-references: UNIPROT:Q40778; UNIPARC:UPI0000126CCE; GB:X78166; NID:g791092; PIDN:
C;Superfamily: fatty acid hydroperoxide lyase

  Query Match             50.5%;  Score 50;  DB 2;  Length 473;
  Best Local Similarity   47.1%;  Pred. No. 11;
  Matches    8;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 YDSIKLEPENPPPYEEA 18
              |:|:::||  || | :|
Db        335 YESLRIEPPVPPQYGKA 351


RESULT 4
AF2165
bicarbonate transport bicarbonate-binding protein cmpA [imported] - Nostoc sp. (strain P
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF2165
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2165
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-458 <KUR>
A;Cross-references: UNIPROT:Q8YT49; UNIPARC:UPI00000CE5BE; GB:BA000019; PIDN:BAB74576.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: cmpA

  Query Match             49.5%;  Score 49;  DB 2;  Length 458;
  Best Local Similarity   50.0%;  Pred. No. 15;
  Matches    7;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 YDSIKLEPENPPPY 15
              :| :| :||||  |
Db        434 FDGVKFDPENPQAY 447


RESULT 5
```

```
T25568
hypothetical protein C24G7.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25568
R;Goela, D.; Wilson, R.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid C24G7.
A;Reference number: Z20052
A;Accession: T25568
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1398 <GOE>
A;Cross-references: UNIPARC:UPI000007AAB2; EMBL:U88310; PIDN:AAB42336.1; GSPDB:GN00019; C
A;Experimental source: strain Bristol N2; clone C24G7
C;Genetics:
A;Gene: CESP:C24G7.5
A;Map position: 1
A;Introns: 13/2; 132/2; 220/3; 316/2; 357/1; 491/3; 558/3; 734/3; 842/1; 1103/3; 1213/2;

  Query Match             49.5%;  Score 49;  DB 2;  Length 1398;
  Best Local Similarity   43.8%;  Pred. No. 54;
  Matches    7;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 YDSIKLEPENPPPYEE 17
              || ::::|: |||  |
Db        263 YDYLRIQPKKPPPTVE 278


RESULT 6
T40240
dimethylase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: T40240
R;Borzym, K.; Beck, A.; Reinhardt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21916
A;Accession: T40240
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-307 <BOR>
A;Cross-references: UNIPROT:Q9USU2; UNIPARC:UPI00001293DF; EMBL:AL121815; PIDN:CAB58154.1
A;Experimental source: strain 972h-; cosmid c336
C;Genetics:
A;Gene: SPDB:SPBC336.02
A;Map position: 2
A;Introns: 45/3
C;Superfamily: dimethyladenosine transferase (rRNA adenosine dimethyltransferase)

  Query Match             49.0%;  Score 48.5;  DB 2;  Length 307;
  Best Local Similarity   50.0%;  Pred. No. 11;
  Matches    8;  Conservative    5;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          5 IKLEPENPPP---YEE 17
              :::||:||||   :||
Db        201 VRIEPKNPPPPLAFEE 216


RESULT 7
T43249
rRNA (adenine-N6,N6-)-dimethyltransferase (EC 2.1.1.-) - fission yeast (Schizosaccharomy
N;Alternate names: dimethylase
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 31-Dec-2004
C;Accession: T43249
R;Housen, I.; Demonte, D.; Lafontaine, D.; Vandenhaute, J.
submitted to the EMBL Data Library, December 1995
A;Description: Cloning and comparative analysis of the SpDIM1 gene from Schizosaccharomy
A;Reference number: Z22366
A;Accession: T43249
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
```

```
A;Residues: 1-315 <HOU>
A;Cross-references: UNIPARC:UPI0000169141; EMBL:Z68293; PIDN:CAA92585.1
C;Genetics:
A;Note: DIM1
C;Function:
A;Description: dimethylation of two adjacent adenosines from the 3' end of the 18SrRNA
C;Superfamily: dimethyladenosine transferase (rRNA adenosine dimethyltransferase)
C;Keywords: methyltransferase

  Query Match             49.0%;  Score 48.5;  DB 2;  Length 315;
  Best Local Similarity   50.0%;  Pred. No. 12;
  Matches    8;  Conservative    5;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          5 IKLEPENPPP---YEE 17
              :::||:||||   :||
Db        201 VRIEPKNPPPPLAFEE 216


RESULT 8
ZNXPLC
zinc finger protein - lymphocytic choriomeningitis virus (strain Armstrong 53b)
C;Species: lymphocytic choriomeningitis virus
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 31-Dec-2004
C;Accession: A32592
R;Salvato, M.S.; Shimomaye, E.M.
Virology 173, 1-10, 1989
A;Title: The completed sequence of lymphocytic choriomeningitis virus reveals a unique R
A;Reference number: A32592; MUID:90051057; PMID:2510401
A;Accession: A32592
A;Molecule type: genomic RNA
A;Residues: 1-90 <SAL>
A;Cross-references: UNIPROT:P18541; UNIPARC:UPI000013C42E; GB:M27693; NID:g331385; PIDN:
C;Comment: This protein may act as an RNA-binding protein.
C;Genetics:
A;Map position: segment L
C;Superfamily: zinc finger protein, Arenaviridae type
C;Keywords: RNA binding; zinc finger
F;32-54/Region: zinc finger CCCC motif

  Query Match             48.5%;  Score 48;  DB 1;  Length 90;
  Best Local Similarity   61.5%;  Pred. No. 3.3;
  Matches    8;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 IKLEPENPPPYEE 17
              |   | :||||||
Db         78 ISTAPSSPPPYEE 90


RESULT 9
F75084
hypothetical protein PAB1661 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F75084
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: F75084
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <KAW>
A;Cross-references: UNIPROT:Q9UZS7; UNIPARC:UPI00000633A9; GB:AJ248286; GB:AL096836; NID
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1661
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB1661

  Query Match             47.5%;  Score 47;  DB 2;  Length 257;
  Best Local Similarity   61.5%;  Pred. No. 15;
  Matches    8;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YDSIKLEPENPPP 14
                ::| ||||:|| |
Db        227 FNSYKLEPKNPVP 239


RESULT 10
T51996
hypothetical protein stil+ - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T51996
R;Yamashita, Y.; Nakaseko, Y.; Samejima, I.; Kumada, K.; Yamada, H.; Yanagida, M.
Nature 384, 276-279, 1996
A;Title: 20S cyclosome complex formation and proteolytic activity inhibited by the cAMP/P
A;Reference number: Z25896
A;Accession: T51996
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-591 <YAM>
A;Cross-references: UNIPROT:Q9USI5; UNIPARC:UPI00001688E4; EMBL:D85197; PIDN:BAA22619.1
C;Genetics:
A;Gene: stil+

  Query Match             47.5%;  Score 47;  DB 2;  Length 591;
  Best Local Similarity   55.6%;  Pred. No. 40;
  Matches   10;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              | || | |  |||| :|
Db        222 SADSAKPETTNPPPQPQA 239


RESULT 11
T41531
activator of Hsp70 and Hsp90 chaperones - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C;Accession: T41531
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z22000
A;Accession: T41531
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-591 <WOO>
A;Cross-references: UNIPROT:Q9USI5; UNIPARC:UPI00001360FA; EMBL:AL049498; PIDN:CAB39910.1
A;Experimental source: strain 972h-; cosmid c645
C;Genetics:
A;Gene: SPDB:SPCC645.14c
A;Map position: 3

  Query Match             47.5%;  Score 47;  DB 2;  Length 591;
  Best Local Similarity   55.6%;  Pred. No. 40;
  Matches   10;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              | || | |  |||| :|
Db        222 SADSAKPETTNPPPQPQA 239


RESULT 12
PC4290
peroxisome proliferator activated receptor gamma 2 - human (fragment)
N;Alternate names: peroxisome proferator activated receptor gamma 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 05-Oct-2004
C;Accession: PC4290
R;Yanase, T.; Yashiro, T.; Takitani, K.; Kato, S.; Taniguchi, S.; Takayanagi, R.; Nawata,
Biochem. Biophys. Res. Commun. 233, 320-324, 1997
A;Title: Differential expression of PPAR gamma 1 and gamma 2 isoforms in human adipose ti
A;Reference number: PC4290; MUID:97289627; PMID:9144532
A;Accession: PC4290
A;Molecule type: mRNA
A;Residues: 1-141 <YAN>
```

A;Cross-references: UNIPARC:UPI000017A1C6; DDBJ:D83136
A;Experimental source: fat
C;Comment: This protein is a nuclear receptor, and plays roles in adipogenesis, adipocyt

  Query Match 46.5%; Score 46; DB 2; Length 141;
  Best Local Similarity 57.1%; Pred. No. 11;
  Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 SIKLEPENPPPYEE 17
:||:|| :|| | |
Db 105 AIKVEPASPPYYSE 118

RESULT 13
T18755
hypothetical protein B0413.7 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18755
R;Basham, V.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19016
A;Accession: T18755
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-156 <WIL>
A;Cross-references: UNIPROT:Q9XTZ7; UNIPARC:UPI0000078CEC; EMBL:Z92824; PIDN:CAB07310.1;
C;Genetics:
A;Gene: CESP:B0413.7
A;Introns: 86/1; 123/1; 149/1

  Query Match 46.5%; Score 46; DB 2; Length 156;
  Best Local Similarity 63.6%; Pred. No. 12;
  Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 SIKLEPENPPP 14
:| :|||||
Db 102 AINFDPENPPP 112

RESULT 14
F89418
protein B0413.7 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89418
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: F89418
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <STO>
A;Cross-references: UNIPROT:Q9XTZ7; UNIPARC:UPI0000078CEC; GB:chr_V; PIDN:CAB07310.1; PI
C;Genetics:
A;Gene: B0413.7
A;Map position: 5

  Query Match 46.5%; Score 46; DB 2; Length 156;
  Best Local Similarity 63.6%; Pred. No. 12;
  Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 SIKLEPENPPP 14
:| :|||||
Db 102 AINFDPENPPP 112

RESULT 15
G83853
spore cortex-lytic enzyme sleB [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83853
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83853
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-330 <STO>
A;Cross-references: UNIPROT:Q9KCE0; UNIPARC:UPI0000135A10; GB:AP001512; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: sleB

  Query Match 46.5%; Score 46; DB 2; Length 330;
  Best Local Similarity 80.0%; Pred. No. 29;
  Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 PENPPPYEEA 18
|| | |||||
Db 184 PEEPTPYEEA 193

Search completed: March 23, 2006, 16:49:13
Job time : 39 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 23, 2006, 16:41:37 ; Search time 229 Seconds
(without alignments)
55.456 Million cell updates/sec

Title: US-09-830-972A-2_COPY_623_640
Perfect score: 99
Sequence: 1 SYDSIKLEPENPPPYEEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	99	100.0	1163	1	RTN4_RAT	Q9jk11 rattus norv
2	95	96.0	578	2	Q80W95_MOUSE	Q80w95 mus musculu
3	95	96.0	639	2	Q8K290_MOUSE	Q8k290 mus musculu
4	95	96.0	720	2	Q7TNB7_MOUSE	Q7tnb7 mus musculu
5	95	96.0	1046	2	Q8BGK7_MOUSE	Q8bgk7 mus musculu
6	95	96.0	1162	2	Q8BGM9_MOUSE	Q8bgm9 mus musculu
7	95	96.0	1163	2	Q8K3G8_MOUSE	Q8k3g8 mus musculu
8	95	96.0	1245	2	Q5DTK9_MOUSE	Q5dtk9 mus musculu
9	85	85.9	818	2	Q53RF4_HUMAN	Q53rf4 homo sapien
10	85	85.9	986	2	Q8IUA4_HUMAN	Q8iua4 homo sapien
11	85	85.9	1192	1	RTN4_HUMAN	Q9nqc3 homo sapien
12	85	85.9	1192	2	Q7L7Q8_HUMAN	Q7l7q8 homo sapien
13	84	84.8	250	2	Q6IG16_PIG	Q6ig16 sus scrofa
14	59	59.6	532	2	Q9PW01_PLEPL	Q9pw01 pleuronecte
15	59	59.6	532	2	Q7T029_PLEPL	Q7t029 pleuronecte
16	59	59.6	532	2	Q9W712_PLAFE	Q9w712 platichthys
17	58	58.6	658	2	Q6RSS8_CHICK	Q6rss8 gallus gall
18	58	58.6	1065	2	Q5MAJ0_CHICK	Q5maj0 gallus gall
19	57	57.6	522	2	Q56TN5_DICLA	Q56tn5 dicentrarch
20	56	56.6	1013	2	Q6JRV9_XENLA	Q6jrv9 xenopus lae
21	56	56.6	1024	2	Q6JRV2_XENLA	Q6jrv2 xenopus lae
22	56	56.6	1032	2	Q6JRV7_XENLA	Q6jrv7 xenopus lae
23	56	56.6	1043	2	Q5JBS0_XENLA	Q5jbs0 xenopus lae
24	56	56.6	1043	2	Q6JRV0_XENLA	Q6jrv0 xenopus lae
25	56	56.6	1044	2	Q6JRV8_XENLA	Q6jrv8 xenopus lae
26	56	56.6	1055	2	Q6JRV1_XENLA	Q6jrv1 xenopus lae
27	54	54.5	188	2	Q60FB8_ONCMY	Q60fb8 oncorhynchu
28	54	54.5	555	2	Q4RX32_TETNG	Q4rx32 tetraodon n
29	54	54.5	2234	2	Q63ZQ9_XENLA	Q63zq9 xenopus lae
30	51	51.5	462	2	Q743Y7_MYCPA	Q743y7 mycobacteri
31	51	51.5	2957	2	O61845_CAEEL	O61845 caenorhabdi
32	50	50.5	358	2	Q6LR12_PHOPR	Q6lr12 photobacter
33	50	50.5	392	2	Q55MP8_CRYNE	Q55mp8 cryptococcu
34	50	50.5	392	2	Q5KB23_CRYNE	Q5kb23 cryptococcu
35	50	50.5	401	2	Q6CEV6_YARLI	Q6cev6 yarrowia li
36	50	50.5	442	2	Q51880_PHOLA	Q51880 phormidium
37	50	50.5	473	1	C74A2_PARAR	Q40778 parthenium
38	50	50.5	515	2	Q8MZ79_DROME	Q8mz79 drosophila
39	50	50.5	814	2	Q57V56_9TRYP	Q57v56 trypanosoma
40	50	50.5	1382	2	Q61EH4_CAEBR	Q61eh4 caenorhabdi
41	49	49.5	212	2	Q5SL11_THET8	Q5sl11 thermus the
42	49	49.5	212	2	Q72LF1_THET2	Q72lf1 thermus the
43	49	49.5	306	1	DIMH_DROME	Q9vaq5 drosophila
44	49	49.5	328	2	Q4L4J3_STAHJ	Q4l4j3 staphylococ
45	49	49.5	335	2	Q4JVJ0_CORJK	Q4jvj0 corynebacte

ALIGNMENTS

```
RESULT 1
RTN4_RAT
ID   RTN4_RAT       STANDARD;      PRT;  1163 AA.
AC   Q9JK11; Q9JK10; Q9R0D9; Q9WUB9; Q9WUF0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE   (Glut4 vesicle 20 kDa protein).
GN   Name=Rtn4; Synonyms=Nogo;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 3), AND PARTIAL PROTEIN SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
RX   MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
RA   Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
RT   "Cloning and characterization of a 22 kDa protein from rat adipocytes:
RT   a new member of the reticulon family.";
RL   Biochim. Biophys. Acta 1450:68-76(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;
RA   Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
RA   Spillmann A.A., Christ F., Schwab M.E.;
RT   "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
RT   antigen for monoclonal antibody IN-1.";
RL   Nature 403:434-439(2000).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 2 AND 4).
RC   STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
RA   Ito T., Schwartz S.M.;
RT   "Cloning of a member of the reticulon gene family in rat: one of two
RT   minor splice variants.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   FUNCTION.
RX   MEDLINE=22033691; PubMed=12037567; DOI=10.1038/417547a;
RA   GrandPre T., Li S., Strittmatter S.M.;
RT   "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
RL   Nature 417:547-551(2002).
CC   -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC       block the regeneration of the nervous central system in adults (By
CC       similarity).
CC   -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC       membrane of the endoplasmic reticulum through 2 putative
CC       transmembrane domains (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
```

```
CC       Name=1; Synonyms=Nogo-A, NI-220-250;
CC         IsoId=Q9JK11-1; Sequence=Displayed;
CC       Name=2; Synonyms=Nogo-B, Foocen-M1;
CC         IsoId=Q9JK11-2; Sequence=VSP_005658;
CC       Name=3; Synonyms=Nogo-C, VP20;
CC         IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
CC       Name=4; Synonyms=Foocen-M2;
CC         IsoId=Q9JK11-4; Sequence=VSP_005659;
CC   -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
CC       nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
CC       present in dorsal root ganglion, sciatic nerve and PC12 cells
CC       after longer exposure. Isoforms 2 and 3 are detected in kidney,
CC       cartilage, skin, lung and spleen. Isoform 3 is expressed at high
CC       level in skeletal muscle. In adult animals isoform 1 is expressed
CC       mainly in the nervous system.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF051335; AAF01564.1; -; mRNA.
DR   EMBL; AJ242961; CAB71027.1; -; mRNA.
DR   EMBL; AJ242962; CAB71028.1; -; mRNA.
DR   EMBL; AJ242963; CAB71029.1; -; mRNA.
DR   EMBL; AF132045; AAD31019.1; -; mRNA.
DR   EMBL; AF132046; AAD31020.1; -; mRNA.
DR   Ensembl; ENSRNOG00000004621; Rattus norvegicus.
DR   GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005635; C:nuclear membrane; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR   GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR   InterPro; IPR003388; Reticulon.
DR   PANTHER; PTHR10994; Reticulon; 1.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Alternative splicing; Direct protein sequencing;
KW   Endoplasmic reticulum; Transmembrane.
FT   TOPO_DOM      1    989       Cytoplasmic (Potential).
FT   TRANSMEM    990   1010       Potential.
FT   TOPO_DOM   1011   1104       Lumenal (Potential).
FT   TRANSMEM   1105   1125       Potential.
FT   TOPO_DOM   1126   1163       Cytoplasmic (Potential).
FT   DOMAIN      976   1163       Reticulon.
FT   COMPBIAS     33     46       Poly-Glu.
FT   COMPBIAS     73     76       Poly-Ala.
FT   COMPBIAS    140    145       Poly-Pro.
FT   VARSPLIC      1    964       Missing (in isoform 3).
FT                                /FTId=VSP_005656.
FT   VARSPLIC    173    975       Missing (in isoform 2).
FT                                /FTId=VSP_005658.
FT   VARSPLIC    192    975       Missing (in isoform 4).
FT                                /FTId=VSP_005659.
FT   VARSPLIC    965    975       AVLSAELSKTS -> MDGQKKHWKDK (in isoform
FT                                3).
FT                                /FTId=VSP_005657.
FT   CONFLICT   1130   1131       Missing (in Ref. 3; AAD31020).
SQ   SEQUENCE   1163 AA;  126388 MW;  8CB894B09E94F0B6 CRC64;

  Query Match             100.0%;  Score 99;  DB 1;  Length 1163;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        623 SYDSIKLEPENPPPYEEA 640


RESULT 2
Q80W95_MOUSE
ID   Q80W95_MOUSE PRELIMINARY;      PRT;   578 AA.
AC   Q80W95;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nogo-A (Fragment).
GN   Name=Rtn4; Synonyms=Nogo-A;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tozaki H., Hirata T.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB073672; BAC75974.1; -; mRNA.
DR   MGI; MGI:1915835; Rtn4.
DR   GO; GO:0042995; C:cell projection; IDA.
DR   GO; GO:0043025; C:cell soma; IDA.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001525; P:angiogenesis; IMP.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   578 AA;  63696 MW;  832670C171E4AC61 CRC64;

  Query Match             96.0%;  Score 95;  DB 2;  Length 578;
  Best Local Similarity   94.4%;  Pred. No. 2.5e-05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||| ||||||||||||||
Db         40 SYDGIKLEPENPPPYEEA 57


RESULT 3
Q8K290_MOUSE
ID   Q8K290_MOUSE PRELIMINARY;      PRT;   639 AA.
AC   Q8K290;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Rtn4 protein.
GN   Name=Rtn4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
```

```
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032192; AAH32192.1; -; mRNA.
DR   MGI; MGI:1915835; Rtn4.
DR   GO; GO:0042995; C:cell projection; IDA.
DR   GO; GO:0043025; C:cell soma; IDA.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001525; P:angiogenesis; IMP.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   639 AA;  70312 MW;  309A19DA37603F11 CRC64;

  Query Match           96.0%;  Score 95;  DB 2;  Length 639;
  Best Local Similarity   94.4%;  Pred. No. 2.8e-05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||| ||||||||||||||||
Db        101 SYDGIKLEPENPPPYEEA 118


RESULT 4
Q7TNB7_MOUSE
ID   Q7TNB7_MOUSE PRELIMINARY;      PRT;   720 AA.
AC   Q7TNB7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   Name=Rtn4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056373; AAH56373.1; -; mRNA.
DR   MGI; MGI:1915835; Rtn4.
DR   GO; GO:0042995; C:cell projection; IDA.
DR   GO; GO:0043025; C:cell soma; IDA.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001525; P:angiogenesis; IMP.
DR   GO; GO:0007399; P:neurogenesis; IDA.
KW   Hypothetical protein.
SQ   SEQUENCE   720 AA;  77435 MW;  80AB78728F16EAB2 CRC64;

  Query Match           96.0%;  Score 95;  DB 2;  Length 720;
  Best Local Similarity   94.4%;  Pred. No. 3.2e-05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||| ||||||||||||||||
Db        624 SYDGIKLEPENPPPYEEA 641


RESULT 5
Q8BGK7_MOUSE
ID   Q8BGK7_MOUSE PRELIMINARY;      PRT;  1046 AA.
AC   Q8BGK7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   RTN4 (Reticulon 4).
GN   Name=Rtn4; ORFNames=RP23-176O5.4-008;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RX   MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA   Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT   "Genomic structure and functional characterisation of the promoters of
RT   human and mouse nogo/rtn4.";
RL   J. Mol. Biol. 325:299-323(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Kay M.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102280; AAM73502.1; -; mRNA.
DR   EMBL; AY102286; AAM73507.1; -; Genomic_DNA.
DR   EMBL; AL929371; CAI24274.1; -; Genomic_DNA.
DR   Ensembl; ENSMUSG00000020458; Mus musculus.
DR   MGI; MGI:1915835; Rtn4.
DR   GO; GO:0042995; C:cell projection; IDA.
DR   GO; GO:0043025; C:cell soma; IDA.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001525; P:angiogenesis; IMP.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   1046 AA;  114221 MW;  8CE2E2238ED51222 CRC64;
```

```
  Query Match             96.0%;  Score 95;  DB 2;  Length 1046;
  Best Local Similarity   94.4%;  Pred. No. 4.9e-05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||| ||||||||||||||
Db        508 SYDGIKLEPENPPPYEEA 525


RESULT 6
Q8BGM9_MOUSE
ID   Q8BGM9_MOUSE PRELIMINARY;      PRT;  1162 AA.
AC   Q8BGM9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   RTN4 (Reticulon 4).
GN   Name=Rtn4; ORFNames=RP23-176O5.4-005;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RX   MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA   Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT   "Genomic structure and functional characterisation of the promoters of
RT   human and mouse nogo/rtn4.";
RL   J. Mol. Biol. 325:299-323(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Kay M.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102284; AAM73506.1; -; mRNA.
DR   EMBL; AY102286; AAM73511.1; -; Genomic_DNA.
DR   EMBL; AL929371; CAI24273.1; -; Genomic_DNA.
DR   Ensembl; ENSMUSG00000020458; Mus musculus.
DR   MGI; MGI:1915835; Rtn4.
DR   GO; GO:0042995; C:cell projection; IDA.
DR   GO; GO:0043025; C:cell soma; IDA.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001525; P:angiogenesis; IMP.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   1162 AA;  126612 MW;  855697FBEE11781F CRC64;

  Query Match             96.0%;  Score 95;  DB 2;  Length 1162;
  Best Local Similarity   94.4%;  Pred. No. 5.5e-05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||| ||||||||||||||
Db        624 SYDGIKLEPENPPPYEEA 641


RESULT 7
Q8K3G8_MOUSE
ID   Q8K3G8_MOUSE PRELIMINARY;      PRT;  1163 AA.
AC   Q8K3G8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Nogo-A.
GN   Name=Rtn4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RA   Jin W., Long M., Li R., Ju G.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY114152; AAM77068.1; -; mRNA.
DR   MGI; MGI:1915835; Rtn4.
DR   GO; GO:0042995; C:cell projection; IDA.
DR   GO; GO:0043025; C:cell soma; IDA.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001525; P:angiogenesis; IMP.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   1163 AA;  126690 MW;  6B5F362799417EA4 CRC64;

  Query Match             96.0%;  Score 95;  DB 2;  Length 1163;
  Best Local Similarity   94.4%;  Pred. No. 5.5e-05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||| ||||||||||||||
Db        624 SYDGIKLEPENPPPYEEA 641


RESULT 8
Q5DTK9_MOUSE
ID   Q5DTK9_MOUSE PRELIMINARY;      PRT;  1245 AA.
AC   Q5DTK9;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   MKIAA4153 protein (Fragment).
GN   Name=Rtn4; Synonyms=mKIAA4153;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Fetal brain;
RA   Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Nagase T., Ohara O.,
RA   Koga H.;
RT   "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene.
RT   The Complete Nucleotide Sequences of Mouse KIAA-homologous cDNAs
RT   Identified by Screening of Terminal sequences of cDNA Clones Randomly
RT   Sampled from Size-Fractionated Libraries. .";
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK220511; BAD90301.1; -; mRNA.
DR   MGI; MGI:1915835; Rtn4.
DR   GO; GO:0042995; C:cell projection; IDA.
DR   GO; GO:0043025; C:cell soma; IDA.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001525; P:angiogenesis; IMP.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
```

```
DR   PROSITE; PS50845; RETICULON; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   1245 AA;  135257 MW;  85460D746CE7F16C CRC64;

  Query Match           96.0%;  Score 95;  DB 2;  Length 1245;
  Best Local Similarity   94.4%;  Pred. No. 6e-05;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||| ||||||||||||||
Db        707 SYDGIKLEPENPPPYEEA 724


RESULT 9
Q53RF4_HUMAN
ID   Q53RF4_HUMAN PRELIMINARY;      PRT;   818 AA.
AC   Q53RF4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein RTN4 (Fragment).
GN   Name=RTN4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kozlowicz A., Wang C.;
RT   "The sequence of Homo sapiens BAC clone RP11-232I22.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.H.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Wilson R.K.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC092461; AAX93116.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
FT   NON_TER     818    818
SQ   SEQUENCE   818 AA;  89515 MW;  A04F9AD5AFDF6433 CRC64;

  Query Match           85.9%;  Score 85;  DB 2;  Length 818;
  Best Local Similarity   83.3%;  Pred. No. 0.0011;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||||
Db        459 NYESIKHEPENPPPYEEA 476


RESULT 10
Q8IUA4_HUMAN
ID   Q8IUA4_HUMAN PRELIMINARY;      PRT;   986 AA.
AC   Q8IUA4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   RNT4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform E) (RTN4 isoform
DE   F) (RTN4 isoform G) (RTN4 isoform Aa).
GN   Name=RTN4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RX   MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA   Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT   "Genomic structure and functional characterisation of the promoters of
RT   human and mouse nogo/rtn4.";
RL   J. Mol. Biol. 325:299-323(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102285; AAM64244.1; -; Genomic_DNA.
DR   EMBL; AY123246; AAM64250.1; -; mRNA.
DR   EMBL; AY123247; AAM64251.1; -; mRNA.
DR   EMBL; AY123248; AAM64252.1; -; mRNA.
DR   EMBL; AY123249; AAM64253.1; -; mRNA.
DR   EMBL; AY123250; AAM64254.1; -; mRNA.
DR   EMBL; AY123245; AAM64249.1; -; mRNA.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   986 AA;  108449 MW;  0CDE8F647036415A CRC64;

  Query Match           85.9%;  Score 85;  DB 2;  Length 986;
  Best Local Similarity   83.3%;  Pred. No. 0.0014;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||||
Db        439 NYESIKHEPENPPPYEEA 456


RESULT 11
RTN4_HUMAN
ID   RTN4_HUMAN     STANDARD;      PRT;  1192 AA.
AC   Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;
AC   Q9Y5U6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE   (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
DE   protein C homolog) (RTN-x) (Reticulon 5).
GN   Name=RTN4; Synonyms=ASY, KIAA0886, NOGO; ORFNames=My043, SP1507;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
RA   Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA   Michalovich D., Simmons D.L., Walsh F.S.;
RT   "Inhibitor of neurite outgrowth in humans.";
RL   Nature 403:383-384(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC   TISSUE=Brain;
RX   MEDLINE=21010696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;
RA   Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
RT   "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
RT   endoplasmic reticulum and reduces their anti-apoptotic activity.";
RL   Oncogene 19:5736-5746(2000).
```

```
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=20237542; PubMed=10773680;
RA   Yang J., Yu L., Bi A.D., Zhao S.-Y.;
RT   "Assignment of the human reticulon 4 gene (RTN4) to chromosome
RT   2p14-->2p13 by radiation hybrid mapping.";
RL   Cytogenet. Cell Genet. 88:101-102(2000).
RN   [4]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 4).
RA   Jin W.-L., Ju G.;
RT   "Developmentally-regulated alternative splicing in a novel Nogo-A.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 2 AND 3).
RC   TISSUE=Placenta, and Skeletal muscle;
RA   Ito T., Schwartz S.M.;
RT   "Cloning of a member of the reticulon gene family in human.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC   TISSUE=Fibroblast;
RA   Yutsudo M.;
RT   "Isolation of a cell death-inducing gene.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 3).
RC   TISSUE=Pituitary;
RA   Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
RA   Luo B., Hu R., Chen J.;
RT   "Human neuroendocrine-specific protein C (NSP) homolog gene.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RX   PubMed=15498874; DOI=10.1073/pnas.0404089101;
RA   Wan D., Gong Y., Qin W., Zhang P., Li J., Wei L., Zhou X., Li H.,
RA   Qiu X., Zhong F., He L., Yu J., Yao G., Jiang H., Qian L., Yu Y.,
RA   Shu H., Chen X., Xu H., Guo M., Pan Z., Chen Y., Ge C., Yang S.,
RA   Gu J.;
RT   "Large-scale cDNA transfection screening for genes related to cancer
RT   development and progression.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:15724-15729(2004).
RN   [9]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=99156230; PubMed=10048485;
RA   Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
RA   Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XII.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 5:355-364(1998).
RN   [10]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 2 AND 3).
RC   TISSUE=Brain, Eye, Ovary, Pancreas, Placenta, and Skeletal muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [11]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC   TISSUE=Umbilical cord blood;
RX   MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;
RA   Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA   Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA   Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT   "Cloning and functional analysis of cDNAs with open reading frames for
RT   300 previously undefined genes expressed in CD34+ hematopoietic
RT   stem/progenitor cells.";
RL   Genome Res. 10:1546-1560(2000).
RN   [12]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 482-1192 (ISOFORMS 1/4).
RC   TISSUE=Petal brain;
RA   Mao Y.M., Xie Y., Zheng Z.H.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [13]
RP   NUCLEOTIDE SEQUENCE OF 186-1192 (ISOFORM 1).
RC   TISSUE=Testis;
RA   Sha J.H., Zhou Z.M., Li J.M.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [14]
RP   TOPOLOGY.
RC   TISSUE=Brain;
RX   MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;
RA   GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
RT   "Identification of the Nogo inhibitor of axon regeneration as a
RT   Reticulon protein.";
RL   Nature 403:439-444(2000).
RN   [15]
RP   FUNCTION.
RC   TISSUE=Brain;
RX   MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
RA   Fournier A.E., GrandPre T., Strittmatter S.M.;
RT   "Identification of a receptor mediating Nogo-66 inhibition of axonal
RT   regeneration.";
RL   Nature 409:341-346(2001).
RN   [16]
RP   REVIEW.
RX   MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134;
RA   Ng C.E.L., Tang B.L.;
RT   "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
RT   regeneration.";
RL   J. Neurosci. Res. 67:559-565(2002).
CC   -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC       block the regeneration of the nervous central system in adults.
CC       Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
CC       This is likely consecutive to their change in subcellular
CC       location, from the mitochondria to the endoplasmic reticulum,
CC       after binding and sequestration.
CC   -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum. Anchored to the membrane of the endoplasmic reticulum
CC       through 2 putative transmembrane domains.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
CC         IsoId=Q9NQC3-1; Sequence=Displayed;
CC       Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
CC         IsoId=Q9NQC3-2; Sequence=VSP_005655;
CC       Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
CC         IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
CC       Name=4;
CC         IsoId=Q9NQC3-4; Sequence=VSP_005654;
CC   -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
CC       and testis and weakly in heart and skeletal muscle. Isoform 2 is
CC       widely expressed excepted for the liver. Isoform 3 is expressed in
CC       brain, skeletal muscle and adipocytes. Isoform 4 is testis-
CC       specific.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   -!- CAUTION: Ref.11 sequence differs from that shown due to
```

```
CC       frameshifts in positions 1149 and 1156.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AJ251383; CAB99248.1; -; mRNA.
DR   EMBL; AJ251384; CAB99249.1; -; mRNA.
DR   EMBL; AJ251385; CAB99250.1; -; mRNA.
DR   EMBL; AB040462; BAB18927.1; -; mRNA.
DR   EMBL; AB040463; BAB18928.1; -; mRNA.
DR   EMBL; AF148537; AAG12176.1; -; mRNA.
DR   EMBL; AF148538; AAG12177.1; -; mRNA.
DR   EMBL; AF087901; AAG12205.1; -; mRNA.
DR   EMBL; AF320999; AAG40878.1; -; mRNA.
DR   EMBL; AF132047; AAD31021.1; -; mRNA.
DR   EMBL; AF132048; AAD31022.1; -; mRNA.
DR   EMBL; AB015639; BAA83712.1; -; mRNA.
DR   EMBL; AF077050; AAD27783.1; -; mRNA.
DR   EMBL; AF177332; AAG17976.1; -; mRNA.
DR   EMBL; AB020693; BAA74909.2; ALT_INIT; mRNA.
DR   EMBL; BC001035; AAH01035.1; -; mRNA.

  Query Match             85.9%;  Score 85;  DB 1;  Length 1192;
  Best Local Similarity   83.3%;  Pred. No. 0.0017;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||
Db        645 NYESIKHEPENPPPYEEA 662


RESULT 12
Q7L7Q8_HUMAN
ID   Q7L7Q8_HUMAN PRELIMINARY;      PRT;  1192 AA.
AC   Q7L7Q8;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   RTN4 isoform A.
GN   Name=RTN4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA   Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT   "Genomic structure and functional characterisation of the promoters of
RT   human and mouse nogo/rtn4.";
RL   J. Mol. Biol. 325:299-323(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102285; AAM64243.1; -; Genomic_DNA.
DR   EMBL; AY102279; AAM64248.1; -; mRNA.
SQ   SEQUENCE   1192 AA;  129930 MW;  CDE239BBF31589CA CRC64;

  Query Match             85.9%;  Score 85;  DB 2;  Length 1192;
  Best Local Similarity   83.3%;  Pred. No. 0.0017;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||
Db        645 NYESIKHEPENPPPYEEA 662


RESULT 13
Q6IG16_PIG
ID   Q6IG16_PIG  PRELIMINARY;      PRT;   250 AA.
AC   Q6IG16;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   RTN4-Aw (Fragment).
GN   Name=RTN4;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22715887; PubMed=12832288;
RA   Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT   "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT   RTN/Nogo gene family.";
RL   FASEB J. 17:1238-1247(2003).
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
DR   EMBL; BK003965; DAA01974.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     250    250
SQ   SEQUENCE   250 AA;  27515 MW;  2E04C47C0FC0424D CRC64;

  Query Match             84.8%;  Score 84;  DB 2;  Length 250;
  Best Local Similarity   93.8%;  Pred. No. 0.00041;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 DSIKLEPENPPPYEEA 18
              :||||||||||||||||
Db          1 ESIKLEPENPPPYEEA 16


RESULT 14
Q9PW01_PLEPL
ID   Q9PW01_PLEPL PRELIMINARY;      PRT;   532 AA.
AC   Q9PW01;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Peroxisome proliferator-activated receptor gamma.
GN   Name=PPAR gamma;
OS   Pleuronectes platessa (Plaice).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Pleuronectoidei; Pleuronectidae; Pleuronectes.
OX   NCBI_TaxID=8262;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Leaver M.J.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR   EMBL; AJ243956; CAB51618.2; -; mRNA.
DR   HSSP; Q96J12; 1NYX.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006350; P:transcription; IEA.
DR   InterPro; IPR000536; Hrmon_recept_lig.
DR   InterPro; IPR001723; Stdhrmn_receptor.
DR   InterPro; IPR000324; VitD_receptor.
DR   InterPro; IPR001628; Znf_C4steroid.
DR   Pfam; PF00104; Hormone_recep; 1.
DR   Pfam; PF00105; zf-C4; 1.
DR   PRINTS; PR00398; STRDHORMONER.
```

```
DR   PRINTS; PR00047; STROIDFINGER.
DR   PRINTS; PR00350; VITAMINDR.
DR   ProDom; PD000035; Znf_C4steroid; 1.
DR   SMART; SM00430; HOLI; 1.
DR   SMART; SM00399; ZnF_C4; 1.
DR   PROSITE; PS00031; NUCLEAR_REC_DBD_1; 1.
KW   DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW   Transcription regulation; Zinc; Zinc-finger.
SQ   SEQUENCE   532 AA;  60410 MW;  19D73F21B3FD9CB8 CRC64;

  Query Match             59.6%;  Score 59;  DB 2;  Length 532;
  Best Local Similarity   52.9%;  Pred. No. 4.8;
  Matches    9;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YDSIKLEPENPPPYEEA 18
              ::|||:|||:|| | ::
Db         97 HNSIKMEPESPPQYSDS 113


RESULT 15
Q7T029_PLEPL
ID   Q7T029_PLEPL PRELIMINARY;      PRT;   532 AA.
AC   Q7T029;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Peroxisome proliferator-activated receptor gamma.
GN   Name=pparg;
OS   Pleuronectes platessa (Plaice).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Pleuronectoidei; Pleuronectidae; Pleuronectes.
OX   NCBI_TaxID=8262;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15790725; DOI=10.1210/en.2004-1638;
RA   Leaver M.J., Boukouvala E., Antonopoulou E., Diez A., Favre-Krey L.,
RA   Ezaz M.T., Bautista J.M., Tocher D.R., Krey G.;
RT   "Three peroxisome proliferator-activated receptor isotypes from each
RT   of two species of marine fish.";
RL   Endocrinology 146:3150-3162(2005).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR   EMBL; AJ539469; CAD62449.1; -; Genomic_DNA.
DR   HSSP; Q96J12; 1I7I.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006350; P:transcription; IEA.
DR   InterPro; IPR001628; Hrmn_rcpt_DNA_bd.
DR   InterPro; IPR000536; Hrmn_rcpt_lig_bd.
DR   InterPro; IPR001723; Stdhrmn_receptor.
DR   InterPro; IPR000324; VitD_receptor.
DR   Pfam; PF00104; Hormone_recep; 1.
DR   Pfam; PF00105; zf-C4; 1.
DR   PRINTS; PR00398; STRDHORMONER.
DR   PRINTS; PR00047; STROIDFINGER.
DR   PRINTS; PR00350; VITAMINDR.
DR   ProDom; PD000035; Znf_C4steroid; 1.
DR   SMART; SM00430; HOLI; 1.
DR   SMART; SM00399; ZnF_C4; 1.
DR   PROSITE; PS00031; NUCLEAR_REC_DBD_1; 1.
DR   PROSITE; PS51030; NUCLEAR_REC_DBD_2; 1.
KW   DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW   Transcription regulation; Zinc; Zinc-finger.
SQ   SEQUENCE   532 AA;  60203 MW;  CA19AEA981B3B406 CRC64;

  Query Match             59.6%;  Score 59;  DB 2;  Length 532;
  Best Local Similarity   52.9%;  Pred. No. 4.8;
  Matches    9;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YDSIKLEPENPPPYEEA 18
              ::|||:|||:|| | ::
Db         97 HNSIKMEPESPPQYSDS 113


Search completed: March 23, 2006, 16:48:29
Job time : 231 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 27, 2006, 06:29:34 ; Search time 190 Seconds
(without alignments)
41.625 Million cell updates/sec

Title: US-09-830-972A-2_COPY_623_640
Perfect score: 99
Sequence: 1 SYDSIKLEPENPPPYEEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	99	100.0	18	3	AAY71335	Aay71335 Bovine P4
2	99	100.0	18	5	ABB81075	Abb81075 Rat Nogo-
3	99	100.0	18	8	ADP45547	Adp45547 Rat NogoA
4	99	100.0	18	9	ADZ07584	Adz07584 Rat NogoA
5	99	100.0	181	3	AAY71400	Aay71400 Rat Nogo
6	99	100.0	356	3	AAY71390	Aay71390 Rat Nogo
7	99	100.0	374	3	AAY71397	Aay71397 Rat Nogo
8	99	100.0	475	3	AAY71389	Aay71389 Rat Nogo
9	99	100.0	502	3	AAY71396	Aay71396 Rat Nogo
10	99	100.0	552	3	AAY71388	Aay71388 Rat Nogo
11	99	100.0	684	3	AAY71394	Aay71394 Rat Nogo
12	99	100.0	695	3	AAY71387	Aay71387 Rat Nogo
13	99	100.0	732	3	AAY71399	Aay71399 Rat Nogo
14	99	100.0	736	3	AAY71398	Aay71398 Rat Nogo
15	99	100.0	737	3	AAY71386	Aay71386 Rat Nogo
16	99	100.0	739	8	ADO26415	Ado26415 Rat trunc
17	99	100.0	746	3	AAY71391	Aay71391 Rat Nogo
18	99	100.0	798	8	ADO26414	Ado26414 Rat trunc
19	99	100.0	803	3	AAY71562	Aay71562 Rat Nogo
20	99	100.0	974	3	AAY71560	Aay71560 Rat Nogo
21	99	100.0	1162	3	AAY71557	Aay71557 Rat Nogo
22	99	100.0	1163	3	AAY71310	Aay71310 Rat neuri
23	99	100.0	1163	3	AAY71384	Aay71384 Alternati
24	99	100.0	1163	5	ABB81074	Abb81074 Rat neuro
25	99	100.0	1163	8	ADO26399	Ado26399 Rat trunc
26	99	100.0	1163	8	ADP45572	Adp45572 Rat NogoA
27	99	100.0	1163	9	ADZ07609	Adz07609 Rat NogoA
28	95	96.0	1162	8	ADT89537	Adt89537 Mus muscu
29	95	96.0	1162	8	ADS99349	Ads99349 Mouse Nog
30	95	96.0	1163	8	ADO08105	Ado08105 Mouse pol
31	85	85.9	18	8	ADP45552	Adp45552 Human Nog
32	85	85.9	18	9	ADZ07589	Adz07589 Human Nog
33	85	85.9	102	6	ADA08167	Ada08167 Nogo-A pr
34	85	85.9	181	8	ADP45570	Adp45570 Human NiG
35	85	85.9	181	9	ADZ07607	Adz07607 Human NiG
36	85	85.9	201	9	AEB08799	Aeb08799 Human NOG
37	85	85.9	642	2	AAW58383	Aaw58383 Human sec
38	85	85.9	642	4	AAB90682	Aab90682 Human BG1
39	85	85.9	819	8	ADP45553	Adp45553 Human NiG
40	85	85.9	819	9	ADZ07590	Adz07590 Human NiG
41	85	85.9	893	3	AAY95012	Aay95012 Human sec
42	85	85.9	960	9	ADY70654	Ady70654 Human BAC
43	85	85.9	983	6	ABU11573	Abu11573 Human MDD
44	85	85.9	1178	3	AAY71311	Aay71311 Human neu
45	85	85.9	1192	3	AAY56967	Aay56967 Human MAG

ALIGNMENTS

RESULT 1
AAY71335
ID AAY71335 standard; peptide; 18 AA.
XX
AC AAY71335;
XX
DT 02-NOV-2000 (first entry)
XX
DE Bovine P472 peptide for antisera production.
XX
KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; P472 peptide; AS 472; antiserum.
XX
OS Bos sp.
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 22; Page 59; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and

CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is a bovine peptide P472 used for antiserum 472 (AS 472) production. This
CC peptide is similar to rat Nogo protein fragment corresponding to residues
CC 623-640 with three mismatches. Note: The present sequence is designated
CC as SEQ ID NO: 33 in the specification. However, in claim 22, SEQ ID NO:
CC 33 is referred as being nucleic acid sequence. SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 99; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 1 SYDSIKLEPENPPPYEEA 18

RESULT 2
ABB81075
ID ABB81075 standard; peptide; 18 AA.
XX
AC ABB81075;
XX
DT 05-NOV-2002 (first entry)
XX
DE Rat Nogo-A p472 peptide (residues 623-640).
XX
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; receptor.
XX
OS Synthetic.
OS Rattus norvegicus.
XX
PN US2002072493-A1.
XX
PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-00893348.
XX
PR 19-MAY-1998; 98IL-00124500.
PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.
PR 19-MAY-1999; 99US-00314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
PS Claim 23; Page 47; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents a peptide
CC fragment of the rat neurotransmitter receptor protein Nogo-A, an example
CC of NS-specific antigen
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 99; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 1 SYDSIKLEPENPPPYEEA 18

RESULT 3
ADP45547
ID ADP45547 standard; peptide; 18 AA.
XX
AC ADP45547;
XX
DT 09-SEP-2004 (first entry)
XX
DE Rat NogoA peptide fragment SEQ ID NO:1.
XX
KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
KW nerve repair; neuroprotective; gene therapy;
KW central nervous system injury; CNS injury; neurodegenerative disorder;
KW rat.
XX
OS Rattus norvegicus.
XX
PN WO2004052932-A2.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-EP013960.
XX
PR 10-DEC-2002; 2002GB-00028832.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
PA (UYZU-) UNIV ZUERICH.
XX
PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;

PI Zurini M;
XX
DR WPI; 2004-468818/44.
XX
PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-
PT D20 or NogoA623-640, useful in preparing a composition for treating CNS
PT injury or neurodegenerative disorders.
XX
PS Example 3; SEQ ID NO 1; 121pp; English.
XX
CC The present invention describes a binding molecule which binds to human
CC NogoA polypeptide, human NiG, human NiG-D20 or human NogoA_623-640 with a
CC dissociation constant of less than 1000nM. Also described: (1) a
CC polynucleotide encoding the binding molecule; (2) an expression vector or
CC system comprising the polynucleotide; (3) a host cell comprising the
CC expression system; (4) a pharmaceutical composition comprising the
CC binding molecule and a carrier or diluent; and (5) treating diseases
CC associated with nerve repair. The binding molecule has neuroprotective
CC activity, and can be used in gene therapy. The binding molecule is useful
CC in preparing a composition for treating central nervous system (CNS)
CC injury or neurodegenerative disorders. The present sequence represents a
CC rat NogoA peptide fragment, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 99; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 1 SYDSIKLEPENPPPYEEA 18

RESULT 4
ADZ07584
ID ADZ07584 standard; peptide; 18 AA.
XX
AC ADZ07584;
XX
DT 16-JUN-2005 (first entry)
XX
DE Rat NogoA_342-357 peptide.
XX
KW antibody; pharmaceutical; peripheral neuropathy;
KW central nervous system disease; neurodegenerative disease;
KW Alzheimers disease; Parkinsons disease; motor neurone disease;
KW ocular disease; diabetic retinopathy; age related macular degeneration;
KW myopia; cns-gen; neuroprotective; nootropic; antiparkinsonian;
KW antidiabetic; ophthalmological; NogoA.
XX
OS Rattus norvegicus.
XX
PN WO2005028508-A2.
XX
PD 31-MAR-2005.
XX
PF 17-SEP-2004; 2004WO-EP010489.
XX
PR 19-SEP-2003; 2003GB-00021997.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
PA (UYZU-) UNIV ZURICH.
XX
PI Barske C, Frentzel S, Mir AK, Schwab ME, Vitaliti A;
XX
DR WPI; 2005-242564/25.
XX
PT New binding molecule capable of binding to human NogoA polypeptide, human
PT NiG, human NiG-D20, or human NogoA342-357, useful for treating nerve
PT repair, Alzheimer's disease, Parkinson's disease, or amyotrophic lateral
PT sclerosis.
XX
PS Disclosure; SEQ ID NO 1; 117pp; English.
XX
CC The invention relates to binding molecules (SEQ ID Nos 2 and 3) capable
CC of binding to human NogoA polypeptide (SEQ ID NO: 5), human NiG
CC polypeptide (SEQ ID NO: 7), human NiG-D20 polypeptide (SEQ ID NO: 24), or
CC human NogoA_342-357 (SEQ ID NO: 6) all given in the specification, with a
CC dissociation constant of less than 1000nM. The binding molecule of the
CC invention comprises a first antigen binding site comprising in sequence
CC the hypervariable regions CDR-H1, CDR-H2, and CDR-H3, where each of the
CC hypervariable regions are at least 50% homologous to their equivalent
CC hypervariable regions CDR-H1-3A6 (SEQ ID NO: 8), CDR-H2-3A6 (SEQ ID NO:
CC 9), and CDR-H3-3A6 (SEQ ID NO: 10) all given in the specification, and a
CC second antigen binding site comprising in sequence the hypervariable
CC regions CDR-L1, CDR-L2, and CDR-L3, where each of the hypervariable
CC regions are at least 50% homologous to their equivalent hypervariable
CC regions CDR-L1-3A6 (SEQ ID NO: 11), CDR-L2-3A6 (SEQ ID NO: 12), and CDR-
CC L3-3A6 (SEQ ID NO: 13) all given in the specification. Also described
CC are: (i) polynucleotide sequences encoding the binding molecules above,
CC (ii) polynucleotide sequences comprising fully defined sequences (SEQ ID
CC Nos 14-19) given in the specification, (iii) an expression vector
CC comprising the polynucleotide sequences above, where the expression
CC system or its part is capable of producing a polypeptide, when the
CC expression system or its part is present in a compatible host cell, (iv)
CC an isolated host cell comprising the expression system above, (v) a
CC pharmaceutical composition comprising the binding molecule in association
CC with at least one pharmaceutical carrier or diluent, and (vi) a method of
CC treating diseases associated with nerve repair. The binding molecules of
CC the invention are useful as a pharmaceutical, preferably in the treatment
CC of nerve repair. They are also useful in the treatment of various
CC diseases of the peripheral (PNS) and central (CNS) nervous system, e.g.
CC neurodegenerative diseases including Alzheimer's disease, Parkinson's
CC disease, or amyotrophic lateral sclerosis. The binding molecules amy also
CC be used for treating degenerative ocular disorders including diabetic
CC retinopathy, age-related macular degeneration, or pathologic myopia. This
CC sequence represents rat NogoA_342-357 peptide. Note: This sequence given
CC as SEQ ID No:1 in the Sequence Listing is not mentioned elsewhere in the
CC specification.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 99; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 1 SYDSIKLEPENPPPYEEA 18

RESULT 5
AAY71400
ID AAY71400 standard; protein; 181 AA.
XX
AC AAY71400;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat Nogo A protein fragment used in the construction of mutant NiG-D20.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.
XX
OS Rattus sp.
XX
PN WO200031235-A2.
XX

PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Example; Page; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is a fragment of rat Nogo A protein shown in AAY71310, which is used in
CC the construction of mutant NiG-D20. NiG-D20 is composed of His-tag/T7-
CC tag/Nogo-A sequence aa 542-722/His-tag. Nogo A deletion mutants were used
CC for mapping the inhibitory sites of Nogo protein. Major inhibitory region
CC was identified in the Nogo A sequence from amino acids 172-974,
CC particularly amino acids 542-722. In addition, N-terminal region 1-171
CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC present sequence is not given in the specification but is derived from
CC rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers
XX
SQ Sequence 181 AA;

Query Match 100.0%; Score 99; DB 3; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 82 SYDSIKLEPENPPPYEEA 99

RESULT 6
AAY71390
ID AAY71390 standard; protein; 356 AA.
XX
AC AAY71390;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat Nogo A protein fragment used in the construction of mutant NiG-D5.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.
XX
OS Rattus sp.
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Example; Page; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is a fragment of rat Nogo A protein shown in AAY71310, which is used in
CC the construction of mutant NiG-D5. NiG-D5 is composed of His-tag/T7-
CC tag/Nogo-A sequence aa 291-646/His-tag. Nogo A deletion mutants were used
CC for mapping the inhibitory sites of Nogo protein. Major inhibitory region
CC was identified in the Nogo A sequence from amino acids 172-974,
CC particularly amino acids 542-722. In addition, N-terminal region 1-171
CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC present sequence is not given in the specification but is derived from
CC rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers
XX
SQ Sequence 356 AA;

Query Match 100.0%; Score 99; DB 3; Length 356;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 333 SYDSIKLEPENPPPYEEA 350

RESULT 7
AAY71397
ID AAY71397 standard; protein; 374 AA.
XX
AC AAY71397;
XX

```
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A protein fragment used in the construction of mutant NiG-D16.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .18
FT                   /note= "Corresponds to residues 172-189 of Nogo A
FT                   sequence shown in AAY71310"
FT   Region          19. .374
FT                   /note= "Corresponds to residues 619-974 of Nogo A
FT                   sequence shown in AAY71310"
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Example; Page; 122pp; English.
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is derived by fusing two fragments of rat Nogo A protein shown in
CC   AAY71310, which is used in the construction of mutant NiG-D16. NiG-D16 is
CC   composed of His-tag/T7-tag/Nogo-A sequence aa 172-189 + 619-974/His-tag.
CC   Nogo A deletion mutants were used for mapping the inhibitory sites of
CC   Nogo protein. Major inhibitory region was identified in the Nogo A
CC   sequence from amino acids 172-974, particularly amino acids 542-722. In
CC   addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
CC   fibroblast spreading. Note: The present sequence is not given in the
CC   specification but is derived from rat Nogo A sequence shown in AAY71310.
CC   SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in
CC   disclosure of the specification. However, the specification does not
CC   include sequences for these SEQ ID numbers
XX
SQ   Sequence 374 AA;

  Query Match           100.0%;  Score 99;  DB 3;  Length 374;
  Best Local Similarity  100.0%;  Pred. No. 7.4e-06;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db         23 SYDSIKLEPENPPPYEEA 40


RESULT 8
AAY71389
ID   AAY71389 standard; protein; 475 AA.
XX
AC   AAY71389;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A protein fragment used in the construction of mutant NiG-D4.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Example; Page; 122pp; English.
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is a fragment of rat Nogo A protein shown in AAY71310, which is used in
CC   the construction of mutant NiG-D4. NiG-D4 is composed of His-tag/T7-
CC   tag/Nogo-A sequence aa 172-646/vector. Nogo A deletion mutants were used
CC   for mapping the inhibitory sites of Nogo protein. Major inhibitory region
CC   was identified in the Nogo A sequence from amino acids 172-974,
CC   particularly amino acids 542-722. In addition, N-terminal region 1-171
```

CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC present sequence is not given in the specification but is derived from
CC rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers
XX
SQ Sequence 475 AA;

Query Match 100.0%; Score 99; DB 3; Length 475;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 452 SYDSIKLEPENPPPYEEA 469

RESULT 9
AAY71396
ID AAY71396 standard; protein; 502 AA.
XX
AC AAY71396;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat Nogo A protein fragment used in the construction of mutant NiG-D15.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Region 1. .18
FT /note= "Corresponds to residues 172-189 of Nogo A
FT sequence shown in AAY71310"
FT Region 19. .502
FT /note= "Corresponds to residues 491-974 of Nogo A
FT sequence shown in AAY71310"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Example; Page; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is derived by fusing two fragments of rat Nogo A protein shown in
CC AAY71310, which is used in the construction of mutant NiG-D15. NiG-D15 is
CC composed of His-tag/T7-tag/Nogo-A sequence aa 172-189 + 491-974/His-tag.
CC Nogo A deletion mutants were used for mapping the inhibitory sites of
CC Nogo protein. Major inhibitory region was identified in the Nogo A
CC sequence from amino acids 172-974, particularly amino acids 542-722. In
CC addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
CC fibroblast spreading. Note: The present sequence is not given in the
CC specification but is derived from rat Nogo A sequence shown in AAY71310.
CC SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in
CC disclosure of the specification. However, the specification does not
CC include sequences for these SEQ ID numbers
XX
SQ Sequence 502 AA;

Query Match 100.0%; Score 99; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 151 SYDSIKLEPENPPPYEEA 168

RESULT 10
AAY71388
ID AAY71388 standard; protein; 552 AA.
XX
AC AAY71388;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat Nogo A protein fragment used in the construction of mutant NiG-D3.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.
XX
OS Rattus sp.
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Example; Page; 122pp; English.

```
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is a fragment of rat Nogo A protein shown in AAY71310, which is used in
CC   the construction of mutant NiG-D3. NiG-D3 is composed of His-tag/T7-
CC   tag/Nogo-A sequence aa 172-723/His-tag. Nogo A deletion mutants were used
CC   for mapping the inhibitory sites of Nogo protein. Major inhibitory region
CC   was identified in the Nogo A sequence from amino acids 172-974,
CC   particularly amino acids 542-722. In addition, N-terminal region 1-171
CC   was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC   present sequence is not given in the specification but is derived from
CC   rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC   in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC   However, the specification does not include sequences for these SEQ ID
CC   numbers
XX
SQ   Sequence 552 AA;

  Query Match             100.0%;  Score 99;  DB 3;  Length 552;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        452 SYDSIKLEPENPPPYEEA 469


RESULT 11
AAY71394
ID   AAY71394 standard; protein; 684 AA.
XX
AC   AAY71394;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A protein fragment used in the construction of mutant NiG-D10.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Example; Page; 122pp; English.
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is a fragment of rat Nogo A protein shown in AAY71310, which is used in
CC   the construction of mutant NiG-D10. NiG-D10 is composed of His-tag/T7-
CC   tag/Nogo-A sequence aa 291-974/His-tag. Nogo A deletion mutants were used
CC   for mapping the inhibitory sites of Nogo protein. Major inhibitory region
CC   was identified in the Nogo A sequence from amino acids 172-974,
CC   particularly amino acids 542-722. In addition, N-terminal region 1-171
CC   was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC   present sequence is not given in the specification but is derived from
CC   rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC   in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC   However, the specification does not include sequences for these SEQ ID
CC   numbers
XX
SQ   Sequence 684 AA;

  Query Match             100.0%;  Score 99;  DB 3;  Length 684;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        333 SYDSIKLEPENPPPYEEA 350


RESULT 12
AAY71387
ID   AAY71387 standard; protein; 695 AA.
XX
AC   AAY71387;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A protein fragment used in the construction of mutant NiG-D2.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
```

```
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Example; Page; 122pp; English.
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is a fragment of rat Nogo A protein shown in AAY71310, which is used in
CC   the construction of mutant NiG-D2. NiG-D2 is composed of His-tag/T7-
CC   tag/Nogo-A sequence aa 172-866/His-tag. Nogo A deletion mutants were used
CC   for mapping the inhibitory sites of Nogo protein. Major inhibitory region
CC   was identified in the Nogo A sequence from amino acids 172-974,
CC   particularly amino acids 542-722. In addition, N-terminal region 1-171
CC   was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC   present sequence is not given in the specification but is derived from
CC   rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC   in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC   However, the specification does not include sequences for these SEQ ID
CC   numbers
XX
SQ   Sequence 695 AA;

  Query Match             100.0%;  Score 99;  DB 3;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        452 SYDSIKLEPENPPPYEEA 469


RESULT 13
AAY71399
ID   AAY71399 standard; protein; 732 AA.
XX
AC   AAY71399;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A protein fragment used in the construction of mutant NiG-D18.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .18
FT                   /note= "Corresponds to residues 172-189 of Nogo A
FT                   sequence shown in AAY71310"
FT   Region          19. .732
FT                   /note= "Corresponds to residues 261-974 of Nogo A
FT                   sequence shown in AAY71310"
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Example; Page; 122pp; English.
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is derived by fusing two fragments of rat Nogo A protein shown in
CC   AAY71310, which is used in the construction of mutant NiG-D18. NiG-D18 is
CC   composed of His-tag/T7-tag/Nogo-A sequence aa 172-189 + 261-974/His-tag.
CC   Nogo A deletion mutants were used for mapping the inhibitory sites of
CC   Nogo protein. Major inhibitory region was identified in the Nogo A
CC   sequence from amino acids 172-974, particularly amino acids 542-722. In
CC   addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
CC   fibroblast spreading. Note: The present sequence is not given in the
CC   specification but is derived from rat Nogo A sequence shown in AAY71310.
CC   SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in
CC   disclosure of the specification. However, the specification does not
CC   include sequences for these SEQ ID numbers
XX
SQ   Sequence 732 AA;

  Query Match             100.0%;  Score 99;  DB 3;  Length 732;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        381 SYDSIKLEPENPPPYEEA 398
```

```
RESULT 14
AAY71398
ID   AAY71398 standard; protein; 736 AA.
XX
AC   AAY71398;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A protein fragment used in the construction of mutant NiG-D17.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .18
FT                   /note= "Corresponds to residues 172-189 of Nogo A
FT                   sequence shown in AAY71310"
FT   Region          19. .736
FT                   /note= "Corresponds to residues 257-974 of Nogo A
FT                   sequence shown in AAY71310"
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME, Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Example; Page; 122pp; English.
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is derived by fusing two fragments of rat Nogo A protein shown in
CC   AAY71310, which is used in the construction of mutant NiG-D17. NiG-D17 is
CC   composed of His-tag/T7-tag/Nogo-A sequence aa 172-189 + 257-974/His-tag.
CC   Nogo A deletion mutants were used for mapping the inhibitory sites of
CC   Nogo protein. Major inhibitory region was identified in the Nogo A
CC   sequence from amino acids 172-974, particularly amino acids 542-722. In
CC   addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
CC   fibroblast spreading. Note: The present sequence is not given in the
CC   specification but is derived from rat Nogo A sequence shown in AAY71310.
CC   SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in
CC   disclosure of the specification. However, the specification does not
CC   include sequences for these SEQ ID numbers
XX
SQ   Sequence 736 AA;

  Query Match             100.0%;  Score 99;  DB 3;  Length 736;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        385 SYDSIKLEPENPPPYEEA 402


RESULT 15
AAY71386
ID   AAY71386 standard; protein; 737 AA.
XX
AC   AAY71386;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A protein fragment used in the construction of mutant NiG-D1.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Example; Page; 122pp; English.
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
```

```
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is a fragment of rat Nogo A protein shown in AAY71310, which is used in
CC   the construction of mutant NiG-D1. NiG-D1 is composed of His-tag/T7-
CC   tag/Nogo-A sequence aa 172-908/vector. Nogo A deletion mutants were used
CC   for mapping the inhibitory sites of Nogo protein. Major inhibitory region
CC   was identified in the Nogo A sequence from amino acids 172-974,
CC   particularly amino acids 542-722. In addition, N-terminal region 1-171
CC   was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC   present sequence is not given in the specification but is derived from
CC   rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC   in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC   However, the specification does not include sequences for these SEQ ID
CC   numbers
XX
SQ   Sequence 737 AA;

  Query Match             100.0%;  Score 99;  DB 3;  Length 737;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        452 SYDSIKLEPENPPPYEEA 469


RESULT 16
ADO26415
ID   ADO26415 standard; protein; 739 AA.
XX
AC   ADO26415;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Rat truncated Nogo-A protein encoded by cDNA vector #1.
XX
KW   rat; human; Nogo-A; truncated; affinity; membrane-bound protein; vector.
XX
OS   Rattus sp.
OS   Synthetic.
XX
PN   WO2004039836-A1.
XX
PD   13-MAY-2004.
XX
PF   31-OCT-2002; 2002WO-EP012210.
XX
PR   31-OCT-2002; 2002WO-EP012210.
XX
PA   (PIER-) PIERIS PROTEOLAB AG.
XX
PI   Skerra A,  Fiedler M;
XX
DR   WPI; 2004-376159/35.
DR   N-PSDB; ADO26411.
XX
PT   New isolated truncated Nogo-A polypeptide that corresponds to a truncated
PT   form of the Nogo-A protein, useful for identifying a compound having
PT   detectable affinity to a Nogo-A protein.
XX
PS   Example 2; Page 75-77; 80pp; English.
XX
CC   The present invention relates to an isolated truncated Nogo-A polypeptide
CC   that corresponds to a truncated form of the Nogo-A protein from the rat
CC   and from the human. The truncated polypeptide is useful for identifying a
CC   compound having detectable affinity to a Nogo-A protein. The present
CC   sequence is a vector encoded Nogo-A protein used in the invention.
XX
SQ   Sequence 739 AA;

  Query Match             100.0%;  Score 99;  DB 8;  Length 739;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        412 SYDSIKLEPENPPPYEEA 429


RESULT 17
AAY71391
ID   AAY71391 standard; protein; 746 AA.
XX
AC   AAY71391;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A protein fragment used in the construction of mutant NiG-D7.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .63
FT                   /note= "Corresponds to residues 172-234 of Nogo A
FT                   sequence shown in AAY71310"
FT   Region          64. .746
FT                   /note= "Corresponds to residues 292-974 of Nogo A
FT                   sequence shown in AAY71310"
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Example; Page; 122pp; English.
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is derived by fusing two fragments of rat Nogo A protein shown in
CC   AAY71310, which is used in the construction of mutant NiG-D7. NiG-D7 is
CC   composed of His-tag/T7-tag/Nogo-A sequence aa 172-234 + 292-974/His-tag.
```

```
CC   Nogo A deletion mutants were used for mapping the inhibitory sites of
CC   Nogo protein. Major inhibitory region was identified in the Nogo A
CC   sequence from amino acids 172-974, particularly amino acids 542-722. In
CC   addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
CC   fibroblast spreading. Note: The present sequence is not given in the
CC   specification but is derived from rat Nogo A sequence shown in AAY71310.
CC   SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in
CC   disclosure of the specification. However, the specification does not
CC   include sequences for these SEQ ID numbers
XX
SQ   Sequence 746 AA;

  Query Match             100.0%;  Score 99;  DB 3;  Length 746;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        395 SYDSIKLEPENPPPYEEA 412


RESULT 18
ADO26414
ID   ADO26414 standard; protein; 798 AA.
XX
AC   ADO26414;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Rat truncated Nogo-A protein encoded by vector pASK111-NiFr2.
XX
KW   rat; human; Nogo-A; truncated; affinity; membrane-bound protein; vector.
XX
OS   Rattus sp.
OS   Synthetic.
XX
PN   WO2004039836-A1.
XX
PD   13-MAY-2004.
XX
PF   31-OCT-2002; 2002WO-EP012210.
XX
PR   31-OCT-2002; 2002WO-EP012210.
XX
PA   (PIER-) PIERIS PROTEOLAB AG.
XX
PI   Skerra A,  Fiedler M;
XX
DR   WPI; 2004-376159/35.
DR   N-PSDB; ADO26412.
XX
PT   New isolated truncated Nogo-A polypeptide that corresponds to a truncated
PT   form of the Nogo-A protein, useful for identifying a compound having
PT   detectable affinity to a Nogo-A protein.
XX
PS   Example 2; Page 72-74; 80pp; English.
XX
CC   The present invention relates to an isolated truncated Nogo-A polypeptide
CC   that corresponds to a truncated form of the Nogo-A protein from the rat
CC   and from the human. The truncated polypeptide is useful for identifying a
CC   compound having detectable affinity to a Nogo-A protein. The present
CC   sequence is a vector encoded Nogo-A protein of the invention.
XX
SQ   Sequence 798 AA;

  Query Match             100.0%;  Score 99;  DB 8;  Length 798;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        471 SYDSIKLEPENPPPYEEA 488


RESULT 19
AAY71562
ID   AAY71562 standard; protein; 803 AA.
XX
AC   AAY71562;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A protein fragment used in the construction of mutant NiG.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Example; Page; 122pp; English.
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is a fragment of rat Nogo A protein shown in AAY71310, which is used in
CC   the construction of mutant NiG. The mutant is composed of His-tag/T7-
CC   tag/Nogo-A sequence aa 172-974/His-tag. Nogo A deletion mutants were used
CC   for mapping the inhibitory sites of Nogo protein. Major inhibitory region
CC   was identified in the Nogo A sequence from amino acids 172-974,
CC   particularly amino acids 542-722. In addition, N-terminal region 1-171
CC   was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC   present sequence is not given in the specification but is derived from
CC   rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC   in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC   However, the specification does not include sequences for these SEQ ID
CC   numbers
XX
SQ   Sequence 803 AA;
```

```
  Query Match             100.0%;  Score 99;  DB 3;  Length 803;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        452 SYDSIKLEPENPPPYEEA 469


RESULT 20
AAY71560
ID   AAY71560 standard; protein; 974 AA.
XX
AC   AAY71560;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A protein fragment used in the construction of mutant NiAext.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Example; Page; 122pp; English.
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is a fragment of rat Nogo A protein shown in AAY71310, which is used in
CC   the construction of mutant NiAext. The mutant is composed of His-tag/T7-
CC   tag/vector/Nogo-A sequence aa 1-974/T7-tag. Nogo A deletion mutants were
CC   used for mapping the inhibitory sites of Nogo protein. Major inhibitory
CC   region was identified in the Nogo A sequence from amino acids 172-974,
CC   particularly amino acids 542-722. In addition, N-terminal region 1-171
CC   was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC   present sequence is not given in the specification but is derived from
CC   rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC   in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC   However, the specification does not include sequences for these SEQ ID
CC   numbers
XX
SQ   Sequence 974 AA;

  Query Match             100.0%;  Score 99;  DB 3;  Length 974;
  Best Local Similarity   100.0%;  Pred. No. 2e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        623 SYDSIKLEPENPPPYEEA 640


RESULT 21
AAY71557
ID   AAY71557 standard; protein; 1162 AA.
XX
AC   AAY71557;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Example; Page; 122pp; English.
XX
CC   The patent relates to neurite growth inhibitor Nogo which is free of all
CC   central nervous system (CNS) myelin material with which it is natively
CC   associated. Nogo proteins and fragments displaying neurite growth
CC   inhibitory activity are used in the treatment of neoplastic disease of
CC   the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC   ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC   oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC   degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC   Therapeutics which promote Nogo activity can be used to treat or prevent
CC   hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC   and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC   used to inhibit production of Nogo protein to induce regeneration of
CC   neurons or to promote structural plasticity of the CNS in disorders where
CC   neurite growth, regeneration or maintenance are deficient or desired. The
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
```

```
CC   treat or prevent disorders or diseases of the CNS. The present sequence
CC   is a truncated form of rat Nogo A protein shown in AAY71310, which is
CC   used in the construction of mutant Nogo-A. Nogo-A is composed of His-
CC   tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were
CC   used for mapping the inhibitory sites of Nogo protein. Major inhibitory
CC   region was identified in the Nogo A sequence from amino acids 172-974,
CC   particularly amino acids 542-722. In addition, N-terminal region 1-171
CC   was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC   present sequence is not given in the specification but is derived from
CC   rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC   in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC   However, the specification does not include sequences for these SEQ ID
CC   numbers
XX
SQ   Sequence 1162 AA;

  Query Match             100.0%;  Score 99;  DB 3;  Length 1162;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        623 SYDSIKLEPENPPPYEEA 640


RESULT 22
AAY71310
ID   AAY71310 standard; protein; 1163 AA.
XX
AC   AAY71310;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat neurite growth inhibitor Nogo A.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Inhibitory-site 1. .171
FT                   /note= "Inhibits NIH 3T3 fibroblast spreading"
FT   Modified-site   30
FT                   /note= "Casein kinase II site"
FT   Region          31. .58
FT                   /note= "Acidic region"
FT   Region          31. .57
FT                   /note= "Region specifically described in claim 16"
FT   Region          172. .259
FT                   /note= "This region is not essential for inhibitory
FT                   activity"
FT   Modified-site   233
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   242. .244
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   291
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   295
FT                   /note= "Protein kinase C (PKC) site"
FT   Misc-difference 404
FT                   /note= "Encoded by TTG"
FT   Modified-site   436
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   468. .470
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   484
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   488
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   502
FT                   /note= "Casein kinase II site"
FT   Inhibitory-site 542. .722
FT   Modified-site   576
FT                   /note= "Casein kinase II site"
FT   Peptide         623. .640
FT                   /note= "used as immunogen to generate antibody AS 472"
FT   Modified-site   626
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   694. .696
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   715
FT                   /note= "Casein kinase II site"
FT   Peptide         762. .1163
FT                   /note= "used as immunogen to generate antibody AS Bruna"
FT   Modified-site   784
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   821
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   850
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   855
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   863
FT                   /note= "Casein kinase II site"
FT   Modified-site   868
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   893
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   912. .914
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   925. .927
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   954
FT                   /note= "PKC and casein kinase II sites"
FT   Modified-site   956
FT                   /note= "PKC and casein kinase II sites"
FT   Region          975. .1162
FT                   /note= "This region is not essential for inhibitory
FT                   activity"
FT   Region          976. .1163
FT                   /note= "C-terminal common region found in Nogo A, B and C
FT                   isoforms"
FT   Domain          988. .1023
FT                   /label= Transmembrane_domain
FT                   /note= "C-terminal hydrophobic region specifically
FT                   described in claim 16"
FT   Modified-site   1024
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   1071. .1073
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   1073
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   1089
FT                   /note= "Protein kinase C (PKC) site"
FT   Domain          1090. .1125
FT                   /label= Transmembrane_domain
FT                   /note= "C-terminal hydrophobic region specifically
FT                   described in claim 16"
FT   Modified-site   1141. .1143
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   1143
FT                   /note= "Protein kinase C (PKC) site"
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US026160.
XX
PR   06-NOV-1998;   98US-0107446P.
```

```
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
DR   N-PSDB; AAD01173.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
XX
PS   Claim 3; Fig 2A; 122pp; English.
XX
CC   The present sequence is a rat Nogo A protein which is a potent neural
CC   cell growth inhibitor and is free of all central nervous system (CNS)
CC   myelin material with which it is natively associated. The protein was
CC   derived from a cDNA generated by fusing RO18U37-3, R1-3U21 cDNAs isolated
CC   from hexanucleotides-primed rat brain stem/spinal cord library, and Oli18
CC   cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins
CC   and fragments displaying neurite growth inhibitory activity are used in
CC   the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC   medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC   haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma,
CC   neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC   Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC   activity can be used to treat or prevent hyperproliferative or benign
CC   dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC   Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC   production of Nogo protein to induce regeneration of neurons or to
CC   promote structural plasticity of the CNS in disorders where neurite
CC   growth, regeneration or maintenance are deficient or desired. The animal
CC   models can be used in diagnostic and screening methods for predisposition
CC   to disorders and to screen for or test molecules which can treat or
CC   prevent disorders or diseases of the CNS. Note: The present sequence
CC   designated as SEQ ID NO: 2 is stated to be the same as the sequence shown
CC   in Fig. 13 (see AAY71384) of the specification. However, this sequence
CC   does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are
CC   referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC   specification. However, the specification does not include sequences for
CC   these SEQ ID numbers
XX
SQ   Sequence 1163 AA;

  Query Match             100.0%;  Score 99;  DB 3;  Length 1163;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        623 SYDSIKLEPENPPPYEEA 640


RESULT 23
AAY71384
ID   AAY71384 standard; protein; 1163 AA.
XX
AC   AAY71384;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Alternative version of rat neurite growth inhibitor Nogo A.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening.
XX
OS   Rattus sp.
XX

FH   Key             Location/Qualifiers
FT   Inhibitory-site 1. .171
FT                   /note= "Inhibits NIH 3T3 fibroblast spreading"
FT   Modified-site   30
FT                   /note= "Casein kinase II site"
FT   Region          31. .58
FT                   /note= "Acidic region"
FT   Region          172. .259
FT                   /note= "This region is not essential for inhibitory
FT                   activity"
FT   Misc-difference 223
FT                   /label= Unknown
FT                   /note= "There is Leu at this position in the sequence
FT                   shown in AAY71310"
FT   Modified-site   233
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   242. .244
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   291
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   295
FT                   /note= "Protein kinase C (PKC) site"
FT   Misc-difference 404
FT                   /note= "There is Ile at this position in the sequence
FT                   shown in AAY71310"
FT   Modified-site   436
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   468. .470
FT                   /note= "Asn is N-glycosylated"
FT   Misc-difference 469
FT                   /label= Unknown
FT                   /note= "There is Lys at this position in the sequence
FT                   shown in AAY71310"
FT   Modified-site   484
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   488
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   502
FT                   /note= "Casein kinase II site"
FT   Inhibitory-site 542. .722
FT   Modified-site   576
FT                   /note= "Casein kinase II site"
FT   Peptide         623. .640
FT                   /note= "used as immunogen to generate antibody AS 472"
FT   Modified-site   626
FT                   /note= "Protein kinase C (PKC) site"
FT   Misc-difference 661
FT                   /note= "There is Asn at this position in the sequence
FT                   shown in AAY71310"
FT   Modified-site   694. .696
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   715
FT                   /note= "Casein kinase II site"
FT   Peptide         762. .1163
FT                   /note= "used as immunogen to generate antibody AS Bruna"
FT   Modified-site   784
FT                   /note= "Protein kinase C (PKC) site"
FT   Misc-difference 820
FT                   /note= "There is Leu at this position in the sequence
FT                   shown in AAY71310"
FT   Modified-site   821
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   850
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   855
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   863
FT                   /note= "Casein kinase II site"
FT   Modified-site   868
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   893
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   912. .914
```

FT /note= "Asn is N-glycosylated"
FT Modified-site 925. .927
FT /note= "Asn is N-glycosylated"
FT Modified-site 954
FT /note= "PKC and casein kinase II sites"
FT Modified-site 956
FT /note= "PKC and casein kinase II sites"
FT Region 975. .1162
FT /note= "This region is not essential for inhibitory
FT activity"
FT Region 976. .1163
FT /note= "C-terminal common region found in Nogo A, B and C
FT isoforms"
FT Domain 988. .1023
FT /label= Transmembrane_domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 1024
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 1071. .1073
FT /note= "Asn is N-glycosylated"
FT Modified-site 1073
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 1089
FT /note= "Protein kinase C (PKC) site"
FT Domain 1090. .1125
FT /label= Transmembrane_domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 1141. .1143
FT /note= "Asn is N-glycosylated"
FT Modified-site 1143
FT /note= "Protein kinase C (PKC) site"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 3; Fig 13; 122pp; English.
XX
CC The present sequence is an alternative version of rat Nogo A protein
CC which is a potent neural cell growth inhibitor and is free of all central
CC nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. Note: The present
CC sequence is an alternative version of the Nogo A sequence shown in Fig.
CC 2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ
CC ID NO: 29 in disclosure of the specification. However the specification
CC does not include sequences for these SEQ ID numbers
XX
SQ Sequence 1163 AA;

Query Match 100.0%; Score 99; DB 3; Length 1163;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 623 SYDSIKLEPENPPPYEEA 640

RESULT 24
ABB81074
ID ABB81074 standard; protein; 1163 AA.
XX
AC ABB81074;
XX
DT 05-NOV-2002 (first entry)
XX
DE Rat neurotransmitter receptor protein Nogo-A.
XX
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; receptor.
XX
OS Rattus norvegicus.
XX
PN US2002072493-A1.
XX
PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-00893348.
XX
PR 19-MAY-1998; 98IL-00124500.
PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.
PR 19-MAY-1999; 99US-00314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR N-PSDB; ABN86600.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
PS Example 5; Page 44-47; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and

```
CC   vitamin deficiency, intervertebral disc herniation, prion diseases such
CC   as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC   neuropathies associated with various diseases, including but not limited
CC   to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC   sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC   amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC   syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC   pathies, complications of various drugs (e.g., metronidazole) and toxins
CC   (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC   telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC   adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC   disease, or lipoproteinemia. The present sequence represents the rat
CC   neurotransmitter receptor protein Nogo-A, an example of NS-specific
CC   antigen
XX
SQ   Sequence 1163 AA;

  Query Match            100.0%;  Score 99;  DB 5;  Length 1163;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        623 SYDSIKLEPENPPPYEEA 640


RESULT 25
ADO26399
ID   ADO26399 standard; protein; 1163 AA.
XX
AC   ADO26399;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Rat truncated Nogo-A protein.
XX
KW   rat; human; Nogo-A; truncated; affinity; membrane-bound protein.
XX
OS   Rattus sp.
XX
PN   WO2004039836-A1.
XX
PD   13-MAY-2004.
XX
PF   31-OCT-2002; 2002WO-EP012210.
XX
PR   31-OCT-2002; 2002WO-EP012210.
XX
PA   (PIER-) PIERIS PROTEOLAB AG.
XX
PI   Skerra A,  Fiedler M;
XX
DR   WPI; 2004-376159/35.
XX
PT   New isolated truncated Nogo-A polypeptide that corresponds to a truncated
PT   form of the Nogo-A protein, useful for identifying a compound having
PT   detectable affinity to a Nogo-A protein.
XX
PS   Claim 1; Fig 6A; 80pp; English.
XX
CC   The present invention relates to an isolated truncated Nogo-A polypeptide
CC   that corresponds to a truncated form of the Nogo-A protein from the rat
CC   and from the human. The truncated polypeptide is useful for identifying a
CC   compound having detectable affinity to a Nogo-A protein. The present
CC   sequence is a Nogo-A polypeptide of the invention.
XX
SQ   Sequence 1163 AA;

  Query Match            100.0%;  Score 99;  DB 8;  Length 1163;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        623 SYDSIKLEPENPPPYEEA 640


RESULT 26
ADP45572
ID   ADP45572 standard; protein; 1163 AA.
XX
AC   ADP45572;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Rat NogoA protein SEQ ID NO:26.
XX
KW   binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
KW   nerve repair; neuroprotective; gene therapy;
KW   central nervous system injury; CNS injury; neurodegenerative disorder;
KW   rat.
XX
OS   Rattus norvegicus.
XX
PN   WO2004052932-A2.
XX
PD   24-JUN-2004.
XX
PF   09-DEC-2003; 2003WO-EP013960.
XX
PR   10-DEC-2002; 2002GB-00028832.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS PHARMA GMBH.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Barske C,  Mir AK,  Oertle T,  Schnell L,  Schwab ME,  Vitaliti A;
PI   Zurini M;
XX
DR   WPI; 2004-468818/44.
DR   N-PSDB; ADP45571.
XX
PT   New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-
PT   D20 or NogoA623-640, useful in preparing a composition for treating CNS
PT   injury or neurodegenerative disorders.
XX
PS   Example 1; SEQ ID NO 26; 121pp; English.
XX
CC   The present invention describes a binding molecule which binds to human
CC   NogoA polypeptide, human NiG, human NiG-D20 or human NogoA_623-640 with a
CC   dissociation constant of less than 1000nM. Also described: (1) a
CC   polynucleotide encoding the binding molecule; (2) an expression vector or
CC   system comprising the polynucleotide; (3) a host cell comprising the
CC   expression system; (4) a pharmaceutical composition comprising the
CC   binding molecule and a carrier or diluent; and (5) treating diseases
CC   associated with nerve repair. The binding molecule has neuroprotective
CC   activity, and can be used in gene therapy. The binding molecule is useful
CC   in preparing a composition for treating central nervous system (CNS)
CC   injury or neurodegenerative disorders. The present sequence represents
CC   rat NogoA, which is used in the exemplification of the present invention.
XX
SQ   Sequence 1163 AA;

  Query Match            100.0%;  Score 99;  DB 8;  Length 1163;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-05;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        623 SYDSIKLEPENPPPYEEA 640


RESULT 27
ADZ07609
ID   ADZ07609 standard; protein; 1163 AA.
XX
```

AC ADZ07609;
XX
DT 16-JUN-2005 (first entry)
XX
DE Rat NogoA polypeptide.
XX
KW antibody; NogoA; pharmaceutical; peripheral neuropathy;
KW central nervous system disease; neurodegenerative disease;
KW Alzheimers disease; Parkinsons disease; motor neurone disease;
KW ocular disease; diabetic retinopathy; age related macular degeneration;
KW myopia; cns-gen; neuroprotective; nootropic; antiparkinsonian;
KW antidiabetic; ophthalmological.
XX
OS Rattus norvegicus.
XX
PN WO2005028508-A2.
XX
PD 31-MAR-2005.
XX
PF 17-SEP-2004; 2004WO-EP010489.
XX
PR 19-SEP-2003; 2003GB-00021997.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
PA (UYZU-) UNIV ZURICH.
XX
PI Barske C, Frentzel S, Mir AK, Schwab ME, Vitaliti A;
XX
DR WPI; 2005-242564/25.
DR N-PSDB; ADZ07608.
XX
PT New binding molecule capable of binding to human NogoA polypeptide, human
PT NiG, human NiG-D20, or human NogoA342-357, useful for treating nerve
PT repair, Alzheimer's disease, Parkinson's disease, or amyotrophic lateral
PT sclerosis.
XX
PS Disclosure; SEQ ID NO 26; 117pp; English.
XX
CC The invention relates to binding molecules (SEQ ID Nos 2 and 3) capable
CC of binding to human NogoA polypeptide (SEQ ID NO: 5), human NiG
CC polypeptide (SEQ ID NO: 7), human NiG-D20 polypeptide (SEQ ID NO: 24), or
CC human NogoA_342-357 (SEQ ID NO: 6) all given in the specification, with a
CC dissociation constant of less than 1000nM. The binding molecule of the
CC invention comprises a first antigen binding site comprising in sequence
CC the hypervariable regions CDR-H1, CDR-H2, and CDR-H3, where each of the
CC hypervariable regions are at least 50% homologous to their equivalent
CC hypervariable regions CDR-H1-3A6 (SEQ ID NO: 8), CDR-H2-3A6 (SEQ ID NO:
CC 9), and CDR-H3-3A6 (SEQ ID NO: 10) all given in the specification, and a
CC second antigen binding site comprising in sequence the hypervariable
CC regions CDR-L1, CDR-L2, and CDR-L3, where each of the hypervariable
CC regions are at least 50% homologous to their equivalent hypervariable
CC regions CDR-L1-3A6 (SEQ ID NO: 11), CDR-L2-3A6 (SEQ ID NO: 12), and CDR-
CC L3-3A6 (SEQ ID NO: 13) all given in the specification. Also described
CC are: (i) polynucleotide sequences encoding the binding molecules above,
CC (ii) polynucleotide sequences comprising fully defined sequences (SEQ ID
CC Nos 14-19) given in the specification, (iii) an expression vector
CC comprising the polynucleotide sequences above, where the expression
CC system or its part is capable of producing a polypeptide, when the
CC expression system or its part is present in a compatible host cell, (iv)
CC an isolated host cell comprising the expression system above, (v) a
CC pharmaceutical composition comprising the binding molecule in association
CC with at least one pharmaceutical carrier or diluent, and (vi) a method of
CC treating diseases associated with nerve repair. The binding molecules of
CC the invention are useful as a pharmaceutical, preferably in the treatment
CC of nerve repair. They are also useful in the treatment of various
CC diseases of the peripheral (PNS) and central (CNS) nervous system, e.g.
CC neurodegenerative diseases including Alzheimer's disease, Parkinson's
CC disease, or amyotrophic lateral sclerosis. The binding molecules amy also
CC be used for treating degenerative ocular disorders including diabetic
CC retinopathy, age-related macular degeneration, or pathologic myopia. This
CC sequence represents rat NogoA polypeptide. Note: This sequence given as
CC SEQ ID No:26 in the Sequence Listing is not mentioned elsewhere in the
CC specification.
XX
SQ Sequence 1163 AA;

Query Match 100.0%; Score 99; DB 9; Length 1163;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 623 SYDSIKLEPENPPPYEEA 640

Search completed: March 27, 2006, 06:32:52
Job time : 192 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 23, 2006, 16:49:28 ; Search time 167 Seconds
(without alignments)
45.035 Million cell updates/sec

Title: US-09-830-972A-2_COPY_623_640
Perfect score: 99
Sequence: 1 SYDSIKLEPENPPPYEEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	99	100.0	18	3	US-09-893-348-19	Sequence 19, Appl
2	99	100.0	18	5	US-10-810-653-19	Sequence 19, Appl
3	99	100.0	1163	3	US-09-893-348-18	Sequence 18, Appl
4	99	100.0	1163	5	US-10-810-653-18	Sequence 18, Appl
5	95	96.0	1162	4	US-10-633-423-10	Sequence 10, Appl
6	95	96.0	1162	4	US-10-427-741-10	Sequence 10, Appl
7	95	96.0	1163	4	US-10-267-502-431	Sequence 431, App
8	85	85.9	1192	3	US-09-789-386-2	Sequence 2, Appli
9	85	85.9	1192	3	US-09-758-140-6	Sequence 6, Appli
10	85	85.9	1192	3	US-09-893-348-23	Sequence 23, Appl
11	85	85.9	1192	3	US-09-972-599A-6	Sequence 6, Appli
12	85	85.9	1192	4	US-10-060-036-71	Sequence 71, Appl
13	85	85.9	1192	4	US-10-408-967-7	Sequence 7, Appli
14	85	85.9	1192	4	US-10-267-502-429	Sequence 429, App
15	85	85.9	1192	4	US-10-327-213-9	Sequence 9, Appli
16	85	85.9	1192	4	US-10-466-258-9	Sequence 9, Appli
17	85	85.9	1192	4	US-10-466-391A-9	Sequence 9, Appli
18	85	85.9	1192	5	US-10-810-653-23	Sequence 23, Appl
19	85	85.9	1192	6	US-11-090-836-3	Sequence 3, Appli
20	85	85.9	1192	6	US-11-090-846-3	Sequence 3, Appli
21	85	85.9	1192	6	US-11-090-847-3	Sequence 3, Appli
22	51	51.5	2957	5	US-10-732-923-8692	Sequence 8692, Ap
23	50	50.5	405	3	US-09-884-260A-54	Sequence 54, Appl
24	50	50.5	473	5	US-10-732-923-9851	Sequence 9851, Ap
25	49	49.5	306	6	US-11-097-143-24576	Sequence 24576, A
26	49	49.5	328	4	US-10-282-122A-71439	Sequence 71439, A
27	49	49.5	1398	4	US-10-369-493-5014	Sequence 5014, Ap
28	48	48.5	104	4	US-10-332-859-188	Sequence 188, App
29	48	48.5	958	4	US-10-437-963-146679	Sequence 146679,
30	48	48.5	1082	4	US-10-437-963-194422	Sequence 194422,
31	47	47.5	61	4	US-10-425-115-359292	Sequence 359292,
32	47	47.5	313	4	US-10-788-792-235	Sequence 235, App
33	47	47.5	591	4	US-10-369-493-22708	Sequence 22708, A
34	47	47.5	591	5	US-10-732-923-9364	Sequence 9364, Ap
35	47	47.5	591	5	US-10-732-923-9365	Sequence 9365, Ap
36	46	46.5	70	4	US-10-424-599-255703	Sequence 255703,
37	46	46.5	232	4	US-10-424-599-253642	Sequence 253642,
38	46	46.5	262	4	US-10-437-963-135251	Sequence 135251,
39	46	46.5	443	4	US-10-305-667A-15	Sequence 15, Appl
40	46	46.5	443	5	US-10-746-592-15	Sequence 15, Appl
41	46	46.5	475	3	US-09-788-070-2	Sequence 2, Appli
42	46	46.5	475	4	US-10-142-373-2	Sequence 2, Appli
43	46	46.5	475	5	US-10-885-977-33	Sequence 33, Appl
44	46	46.5	477	4	US-10-190-264-1	Sequence 1, Appli
45	46	46.5	477	5	US-10-723-860-1496	Sequence 1496, Ap

ALIGNMENTS

RESULT 1
US-09-893-348-19
; Sequence 19, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-19

Query Match 100.0%; Score 99; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 1 SYDSIKLEPENPPPYEEA 18

RESULT 2
US-10-810-653-19
; Sequence 19, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

```
;  FILE REFERENCE: EIS-SCHWARTZ=2A
;  CURRENT APPLICATION NUMBER: US/10/810,653
;  CURRENT FILING DATE:  2004-03-29
;  PRIOR APPLICATION NUMBER: US/09/893,348
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/314,161
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: US 09/218,277
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: PCT/US98/14715
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-810-653-19

  Query Match           100.0%;  Score 99;  DB 5;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-06;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db          1 SYDSIKLEPENPPPYEEA 18


RESULT 3
US-09-893-348-18
; Sequence 18, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
;  APPLICANT: EISENBACH-SCHWARTZ, Michal
;  APPLICANT:  COHEN, Irun R.
;  APPLICANT:  BESERMAN, Pierre
;  APPLICANT:  MOSONEGO, Alon
;  APPLICANT:  MOALEM, Gila
;  TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
;  FILE REFERENCE: EIS-SCHWARTZ=2A
;  CURRENT APPLICATION NUMBER: US/09/893,348
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/314,161
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: US 09/218,277
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: PCT/US98/14715
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 1163
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-893-348-18

  Query Match           100.0%;  Score 99;  DB 3;  Length 1163;
  Best Local Similarity  100.0%;  Pred. No. 0.00023;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        623 SYDSIKLEPENPPPYEEA 640


RESULT 4
US-10-810-653-18
; Sequence 18, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
;  APPLICANT: EISENBACH-SCHWARTZ, Michal
;  APPLICANT:  COHEN, Irun R.
;  APPLICANT:  BESERMAN, Pierre
;  APPLICANT:  MOSONEGO, Alon
;  APPLICANT:  MOALEM, Gila
;  TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
;  FILE REFERENCE: EIS-SCHWARTZ=2A
;  CURRENT APPLICATION NUMBER: US/10/810,653
;  CURRENT FILING DATE:  2004-03-29
;  PRIOR APPLICATION NUMBER: US/09/893,348
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/314,161
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: US 09/218,277
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: PCT/US98/14715
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 1163
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-810-653-18

  Query Match           100.0%;  Score 99;  DB 5;  Length 1163;
  Best Local Similarity  100.0%;  Pred. No. 0.00023;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        623 SYDSIKLEPENPPPYEEA 640


RESULT 5
US-10-633-423-10
; Sequence 10, Application US/10633423
; Publication No. US20040191240A1
; GENERAL INFORMATION:
;  APPLICANT: Tohyama, Masaya
;  APPLICANT:  Yamashita, Toshihide
;  TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
;  FILE REFERENCE: 59150-8023.US00
;  CURRENT APPLICATION NUMBER: US/10/633,423
;  CURRENT FILING DATE:  2003-07-11
;  PRIOR APPLICATION NUMBER: US 10/427,741
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: JP 2003-92923
;  PRIOR FILING DATE: 2003-03-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 1162
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-633-423-10

  Query Match           96.0%;  Score 95;  DB 4;  Length 1162;
  Best Local Similarity  94.4%;  Pred. No. 0.00078;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||| ||||||||||||||
Db        624 SYDGIKLEPENPPPYEEA 641


RESULT 6
US-10-427-741-10
; Sequence 10, Application US/10427741
; Publication No. US20040191291A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Tohyama, Masaya
;  APPLICANT:  Yamashita, Toshihide
;  TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
;  FILE REFERENCE: 59150-8023
;  CURRENT APPLICATION NUMBER: US/10/427,741
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: JP 2003-92923
;  PRIOR FILING DATE: 2003-03-28
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 1162
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-427-741-10

  Query Match             96.0%;  Score 95;  DB 4;  Length 1162;
  Best Local Similarity   94.4%;  Pred. No. 0.00078;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||| ||||||||||||||||
Db        624 SYDGIKLEPENPPPYEEA 641


RESULT 7
US-10-267-502-431
; Sequence 431, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
;  APPLICANT: Kim, Jaeseob
;  APPLICANT:  Galant, Ron
;  TITLE OF INVENTION: Obesity Linked Genes
;  FILE REFERENCE: LSD-07416
;  CURRENT APPLICATION NUMBER: US/10/267,502
;  CURRENT FILING DATE:  2003-01-27
;  NUMBER OF SEQ ID NOS: 439
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 431
;   LENGTH: 1163
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-267-502-431

  Query Match             96.0%;  Score 95;  DB 4;  Length 1163;
  Best Local Similarity   94.4%;  Pred. No. 0.00078;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||| ||||||||||||||||
Db        624 SYDGIKLEPENPPPYEEA 641


RESULT 8
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
;  APPLICANT: MICHALOVICH, DAVID
;  APPLICANT:  PRINJHA, RABINDER KUMAR
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP-30165-C1
;  CURRENT APPLICATION NUMBER: US/09/789,386
;  CURRENT FILING DATE:  2001-02-21
;  PRIOR APPLICATION NUMBER: U.K. 9916898.1
;  PRIOR FILING DATE: 1999-07-19
;  PRIOR APPLICATION NUMBER: U.K. 9816024.5
;  PRIOR FILING DATE: 1998-07-22
;  PRIOR APPLICATION NUMBER: US 09/359,208
;  PRIOR FILING DATE: 1999-07-22
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-789-386-2

  Query Match             85.9%;  Score 85;  DB 3;  Length 1192;
  Best Local Similarity   83.3%;  Pred. No. 0.016;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||||
Db        645 NYESIKHEPENPPPYEEA 662


RESULT 9
US-09-758-140-6
; Sequence 6, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
;  APPLICANT:  Strittmatter, Stephen M.
;  TITLE OF INVENTION:  No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
;  FILE REFERENCE:  44574-5073-US
;  CURRENT APPLICATION NUMBER: US/09/758,140
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER:  US 60/175,707
;  PRIOR FILING DATE:  2000-01-12
;  PRIOR APPLICATION NUMBER:  US 60/207,366
;  PRIOR FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  US 60/236,378
;  PRIOR FILING DATE:  2000-09-29
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-758-140-6

  Query Match             85.9%;  Score 85;  DB 3;  Length 1192;
  Best Local Similarity   83.3%;  Pred. No. 0.016;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||||
Db        645 NYESIKHEPENPPPYEEA 662


RESULT 10
US-09-893-348-23
; Sequence 23, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
;  APPLICANT: EISENBACH-SCHWARTZ, Michal
;  APPLICANT:  COHEN, Irun R.
;  APPLICANT:  BESERMAN, Pierre
;  APPLICANT:  MOSONEGO, Alon
;  APPLICANT:  MOALEM, Gila
;  TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
;  FILE REFERENCE: EIS-SCHWARTZ=2A
;  CURRENT APPLICATION NUMBER: US/09/893,348
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/314,161
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: US 09/218,277
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: PCT/US98/14715
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
```

```
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-893-348-23

  Query Match             85.9%;  Score 85;  DB 3;  Length 1192;
  Best Local Similarity   83.3%;  Pred. No. 0.016;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||||
Db        645 NYESIKHEPENPPPYEEA 662


RESULT 11
US-09-972-599A-6
; Sequence 6, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
;  APPLICANT: STRITTMATTER, STEPHEN M.
;  TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
;  FILE REFERENCE: C077 CIP US
;  CURRENT APPLICATION NUMBER: US/09/972,599A
;  CURRENT FILING DATE:  2001-10-06
;  PRIOR APPLICATION NUMBER: PCT/US01/01041
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: 09/758,140
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: 60/236,378
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: 60/207,366
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/175,707
;  PRIOR FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-972-599A-6

  Query Match             85.9%;  Score 85;  DB 3;  Length 1192;
  Best Local Similarity   83.3%;  Pred. No. 0.016;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||||
Db        645 NYESIKHEPENPPPYEEA 662


RESULT 12
US-10-060-036-71
; Sequence 71, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Persing, David H.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Jiang, Yuqiu
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF PANCREATIC CANCER
;  FILE REFERENCE: 210121.566
;  CURRENT APPLICATION NUMBER: US/10/060,036
;  CURRENT FILING DATE:  2002-01-30
;  NUMBER OF SEQ ID NOS: 4560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-060-036-71

  Query Match             85.9%;  Score 85;  DB 4;  Length 1192;
  Best Local Similarity   83.3%;  Pred. No. 0.016;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||||
Db        645 NYESIKHEPENPPPYEEA 662


RESULT 13
US-10-408-967-7
; Sequence 7, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia & Upjohn Company
;  APPLICANT:  Yan, Riqiang
;  APPLICANT:  Lu, Yifeng
;  TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
;  FILE REFERENCE: 00925
;  CURRENT APPLICATION NUMBER: US/10/408,967
;  CURRENT FILING DATE:  2003-04-08
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-967-7

  Query Match             85.9%;  Score 85;  DB 4;  Length 1192;
  Best Local Similarity   83.3%;  Pred. No. 0.016;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||||
Db        645 NYESIKHEPENPPPYEEA 662


RESULT 14
US-10-267-502-429
; Sequence 429, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
;  APPLICANT: Kim, Jaeseob
;  APPLICANT:  Galant, Ron
;  TITLE OF INVENTION: Obesity Linked Genes
;  FILE REFERENCE: LSD-07416
;  CURRENT APPLICATION NUMBER: US/10/267,502
;  CURRENT FILING DATE:  2003-01-27
;  NUMBER OF SEQ ID NOS: 439
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-267-502-429

  Query Match             85.9%;  Score 85;  DB 4;  Length 1192;
  Best Local Similarity   83.3%;  Pred. No. 0.016;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||||
Db        645 NYESIKHEPENPPPYEEA 662


RESULT 15
US-10-327-213-9
; Sequence 9, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
```

; APPLICANT: PILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-213-9

Query Match 85.9%; Score 85; DB 4; Length 1192;
Best Local Similarity 83.3%; Pred. No. 0.016;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||
Db        645 NYESIKHEPENPPPYEEA 662
```

Search completed: March 23, 2006, 16:52:58
Job time : 168 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 23, 2006, 16:50:18 ; Search time 23 Seconds
(without alignments)
22.401 Million cell updates/sec

Title: US-09-830-972A-2_COPY_623_640
Perfect score: 99
Sequence: 1 SYDSIKLEPENPPPYEEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	99	100.0	18	7	US-11-044-899-33	Sequence 33, Appl
2	99	100.0	1163	7	US-11-044-899-2	Sequence 2, Appli
3	99	100.0	1163	7	US-11-044-899-30	Sequence 30, Appl
4	85	85.9	201	7	US-11-177-648-76	Sequence 76, Appl
5	85	85.9	1178	7	US-11-044-899-29	Sequence 29, Appl
6	80	80.8	200	7	US-11-177-648-113	Sequence 113, App
7	46	46.5	247	7	US-11-096-568A-28475	Sequence 28475, A
8	46	46.5	329	7	US-11-096-568A-28474	Sequence 28474, A
9	46	46.5	340	7	US-11-096-568A-28473	Sequence 28473, A
10	46	46.5	505	6	US-10-519-447-4	Sequence 4, Appli
11	46	46.5	688	7	US-11-106-674-1	Sequence 1, Appli
12	45	45.5	487	7	US-11-249-847-582	Sequence 582, App
13	44	44.4	361	7	US-11-096-568A-28287	Sequence 28287, A
14	44	44.4	363	7	US-11-096-568A-28286	Sequence 28286, A
15	44	44.4	413	7	US-11-096-568A-28285	Sequence 28285, A
16	44	44.4	569	7	US-11-096-568A-23878	Sequence 23878, A
17	44	44.4	584	7	US-11-096-568A-23877	Sequence 23877, A
18	44	44.4	605	7	US-11-096-568A-23876	Sequence 23876, A
19	43	43.4	206	7	US-11-015-546A-7	Sequence 7, Appli
20	43	43.4	212	7	US-11-015-546A-5	Sequence 5, Appli
21	43	43.4	219	7	US-11-015-546A-4	Sequence 4, Appli
22	43	43.4	253	7	US-11-015-546A-2	Sequence 2, Appli
23	43	43.4	269	7	US-11-015-546A-10	Sequence 10, Appl
24	43	43.4	274	7	US-11-015-546A-12	Sequence 12, Appl
25	43	43.4	473	7	US-11-096-568A-7408	Sequence 7408, Ap
26	43	43.4	491	7	US-11-096-568A-9195	Sequence 9195, Ap
27	43	43.4	491	7	US-11-096-568A-9196	Sequence 9196, Ap
28	43	43.4	493	7	US-11-096-568A-9194	Sequence 9194, Ap
29	43	43.4	511	7	US-11-096-568A-9193	Sequence 9193, Ap
30	43	43.4	601	7	US-11-103-957-3	Sequence 3, Appli
31	43	43.4	601	7	US-11-018-868-119	Sequence 119, App
32	41.5	41.9	243	6	US-10-511-538-95	Sequence 95, Appl
33	41.5	41.9	243	6	US-10-537-002-66	Sequence 66, Appl
34	41	41.4	195	6	US-10-995-561-563	Sequence 563, App
35	41	41.4	236	7	US-11-096-568A-10192	Sequence 10192, A
36	41	41.4	251	7	US-11-096-568A-10191	Sequence 10191, A
37	41	41.4	470	7	US-11-024-959-297	Sequence 297, App
38	41	41.4	954	7	US-11-096-568A-31293	Sequence 31293, A
39	41	41.4	959	7	US-11-096-568A-28237	Sequence 28237, A
40	41	41.4	963	7	US-11-096-568A-31292	Sequence 31292, A
41	41	41.4	964	7	US-11-096-568A-31291	Sequence 31291, A
42	41	41.4	968	7	US-11-096-568A-28236	Sequence 28236, A
43	41	41.4	1375	6	US-10-995-561-809	Sequence 809, App
44	41	41.4	1376	7	US-11-100-640-32	Sequence 32, Appl
45	40.5	40.9	163	7	US-11-096-568A-17369	Sequence 17369, A

ALIGNMENTS

RESULT 1
US-11-044-899-33
; Sequence 33, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; TITLE OF INVENTION: THEREON
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Bos sp.
US-11-044-899-33

Query Match 100.0%; Score 99; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSIKLEPENPPPYEEA 18
||||||||||||||||||
Db 1 SYDSIKLEPENPPPYEEA 18

RESULT 2
US-11-044-899-2
; Sequence 2, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; TITLE OF INVENTION: THEREON
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972

```
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: PCT/US99/26160
;  PRIOR FILING DATE: 1999-11-05
;  PRIOR APPLICATION NUMBER: 60/107,446
;  PRIOR FILING DATE: 1998-11-06
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 1163
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-11-044-899-2

  Query Match             100.0%;  Score 99;  DB 7;  Length 1163;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-07;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        623 SYDSIKLEPENPPPYEEA 640


RESULT 3
US-11-044-899-30
; Sequence 30, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
;  APPLICANT: Schwab, M.
;  APPLICANT:  Chen, M.
;  TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
;  TITLE OF INVENTION:  THEREON
;  FILE REFERENCE: 10200-017-999
;  CURRENT APPLICATION NUMBER: US/11/044,899
;  CURRENT FILING DATE:  2005-01-26
;  PRIOR APPLICATION NUMBER: 09/830,972
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: PCT/US99/26160
;  PRIOR FILING DATE: 1999-11-05
;  PRIOR APPLICATION NUMBER: 60/107,446
;  PRIOR FILING DATE: 1998-11-06
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
;   LENGTH: 1163
;   TYPE: PRT
;   ORGANISM: Rattus sp.
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1163) at all Xaa position
;   OTHER INFORMATION: Xaa = any amino acid
US-11-044-899-30

  Query Match             100.0%;  Score 99;  DB 7;  Length 1163;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-07;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              ||||||||||||||||||
Db        623 SYDSIKLEPENPPPYEEA 640


RESULT 4
US-11-177-648-76
; Sequence 76, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
;  APPLICANT: Jonathon Henry ELLIS
;  APPLICANT:  Paul Andrew HAMBLIN
;  APPLICANT:  Paul Alexander WILSON
;  APPLICANT:  Alan Peter LEWIS
;  TITLE OF INVENTION: IMMUNOGLOBULINS
;  FILE REFERENCE: PB60608-2
;  CURRENT APPLICATION NUMBER: US/11/177,648
;  CURRENT FILING DATE:  2005-07-06
;  PRIOR APPLICATION NUMBER: PCT/GB2004/005325
;  PRIOR FILING DATE: 2004-12-20
;  PRIOR APPLICATION NUMBER: GB0329711.6
;  PRIOR FILING DATE: 2003-12-22
;  PRIOR APPLICATION NUMBER: GB0329684.5
;  PRIOR FILING DATE: 2003-12-22
;  NUMBER OF SEQ ID NOS: 113
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Amino acids 586-785 of human NOGO A (NOGO-A56)
US-11-177-648-76

  Query Match             85.9%;  Score 85;  DB 7;  Length 201;
  Best Local Similarity   83.3%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||
Db         60 NYESIKHEPENPPPYEEA 77


RESULT 5
US-11-044-899-29
; Sequence 29, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
;  APPLICANT: Schwab, M.
;  APPLICANT:  Chen, M.
;  TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
;  TITLE OF INVENTION:  THEREON
;  FILE REFERENCE: 10200-017-999
;  CURRENT APPLICATION NUMBER: US/11/044,899
;  CURRENT FILING DATE:  2005-01-26
;  PRIOR APPLICATION NUMBER: 09/830,972
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: PCT/US99/26160
;  PRIOR FILING DATE: 1999-11-05
;  PRIOR APPLICATION NUMBER: 60/107,446
;  PRIOR FILING DATE: 1998-11-06
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
;   LENGTH: 1178
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1178) at all Xaa position
;   OTHER INFORMATION: Xaa = any amino acid
US-11-044-899-29

  Query Match             85.9%;  Score 85;  DB 7;  Length 1178;
  Best Local Similarity   83.3%;  Pred. No. 7.8e-05;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :|:||| ||||||||||
Db        631 NYESIKHEPENPPPYEEA 648


RESULT 6
US-11-177-648-113
; Sequence 113, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
;  APPLICANT: Jonathon Henry ELLIS
;  APPLICANT:  Paul Andrew HAMBLIN
;  APPLICANT:  Paul Alexander WILSON
```

```
;  APPLICANT:  Alan Peter LEWIS
;  TITLE OF INVENTION: IMMUNOGLOBULINS
;  FILE REFERENCE: PB60608-2
;  CURRENT APPLICATION NUMBER: US/11/177,648
;  CURRENT FILING DATE:  2005-07-06
;  PRIOR APPLICATION NUMBER: PCT/GB2004/005325
;  PRIOR FILING DATE: 2004-12-20
;  PRIOR APPLICATION NUMBER: GB0329711.6
;  PRIOR FILING DATE: 2003-12-22
;  PRIOR APPLICATION NUMBER: GB0329684.5
;  PRIOR FILING DATE: 2003-12-22
;  NUMBER OF SEQ ID NOS: 113
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 113
;   LENGTH: 200
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Amino acid sequence of Marmoset NOGO-A fragment
US-11-177-648-113

  Query Match             80.8%;  Score 80;  DB 7;  Length 200;
  Best Local Similarity   72.2%;  Pred. No. 6.2e-05;
  Matches   13;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENPPPYEEA 18
              :::|:| ||||||||||
Db         60 NFESVKHEPENPPPYEEA 77


RESULT 7
US-11-096-568A-28475
; Sequence 28475, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28475
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(247)
;   OTHER INFORMATION: Ceres Seq. ID no. 2996848
US-11-096-568A-28475

  Query Match             46.5%;  Score 46;  DB 7;  Length 247;
  Best Local Similarity   69.2%;  Pred. No. 9;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 IKLEPENPPPYEE 17
              | | ||||| | |
Db         40 IHLWPENPPGYRE 52


RESULT 8
US-11-096-568A-28474
; Sequence 28474, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28474
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(329)
;   OTHER INFORMATION: Ceres Seq. ID no. 2996847
US-11-096-568A-28474

  Query Match             46.5%;  Score 46;  DB 7;  Length 329;
  Best Local Similarity   69.2%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 IKLEPENPPPYEE 17
              | | ||||| | |
Db        122 IHLWPENPPGYRE 134


RESULT 9
US-11-096-568A-28473
; Sequence 28473, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28473
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(340)
;   OTHER INFORMATION: Ceres Seq. ID no. 2996846
US-11-096-568A-28473

  Query Match             46.5%;  Score 46;  DB 7;  Length 340;
  Best Local Similarity   69.2%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 IKLEPENPPPYEE 17
              | | ||||| | |
Db        133 IHLWPENPPGYRE 145


RESULT 10
US-10-519-447-4
; Sequence 4, Application US/10519447
; Publication No. US20050244829A1
; GENERAL INFORMATION:
;  APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
;  APPLICANT:  Makoto OGINO
;  APPLICANT:  Hideki ENDOH
;  TITLE OF INVENTION: METHOD FOR SCREENING AN AGENT FOR IMPROVING INSULIN RESISTANCE
;  FILE REFERENCE: Q85576
;  CURRENT APPLICATION NUMBER: US/10/519,447
;  CURRENT FILING DATE:  2004-12-30
;  PRIOR APPLICATION NUMBER: PCT/JP03/08367
;  PRIOR FILING DATE: 2003-07-01
;  PRIOR APPLICATION NUMBER: JP 2002-193814
;  PRIOR FILING DATE: 2002-07-02
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 505
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-519-447-4
```

```
  Query Match             46.5%;  Score 46;  DB 6;  Length 505;
  Best Local Similarity   57.1%;  Pred. No. 20;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db        105 AIKVEPASPPYYSE 118


RESULT 11
US-11-106-674-1
; Sequence 1, Application US/11106674
; Publication No. US20050289658A1
; GENERAL INFORMATION:
;  APPLICANT: Aventis Pharma S.A.
;  TITLE OF INVENTION: SYSTEM FOR REGULATING IN VIVO THE EXPRESSION OF A TRANSGENE BY
;  TITLE OF INVENTION:  CONDITIONAL INHIBITION
;  FILE REFERENCE: 03806.0512
;  CURRENT APPLICATION NUMBER: US/11/106,674
;  CURRENT FILING DATE:  2005-04-15
;  PRIOR APPLICATION NUMBER: US/09/931,007
;  PRIOR FILING DATE: 2001-08-17
;  PRIOR APPLICATION NUMBER: FR 00/10730
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: US 60/239,246
;  PRIOR FILING DATE: 2000-10-11
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 688
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc
;   LOCATION: (1)..(688)
;   OTHER INFORMATION: Sequence for PPAR-gamma-2-gamma-2, a modified human PPAR-gamma (P
;   OTHER INFORMATION: eroxisome Proliferator Activated Receptor-gamma)
US-11-106-674-1

  Query Match             46.5%;  Score 46;  DB 7;  Length 688;
  Best Local Similarity   57.1%;  Pred. No. 27;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db        105 AIKVEPASPPYYSE 118


RESULT 12
US-11-249-847-582
; Sequence 582, Application US/11249847
; Publication No. US20060035270A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Frank D.
;  APPLICANT:  Meng, Dr. Xun
;  APPLICANT:  Chan, John W.
;  APPLICANT:  Zhang, Shengsheng
;  APPLICANT:  Benkovic, Stephen J.
;  TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN
;  TITLE OF INVENTION:  PROTEIN ANALYSIS
;  FILE REFERENCE: EPTM-P05-001
;  CURRENT APPLICATION NUMBER: US/11/249,847
;  CURRENT FILING DATE:  2005-10-12
;  PRIOR APPLICATION NUMBER: 10/436,549
;  PRIOR FILING DATE: 2003-05-12
;  PRIOR APPLICATION NUMBER: 60/379,626
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/393,137
;  PRIOR FILING DATE: 2002-07-01
;  PRIOR APPLICATION NUMBER: 60/393,197
;  PRIOR FILING DATE: 2002-07-01
;  PRIOR APPLICATION NUMBER: 60/393,211
;  PRIOR FILING DATE: 2002-07-01
;  PRIOR APPLICATION NUMBER: 60/393,223
;  PRIOR FILING DATE: 2002-07-01
;  PRIOR APPLICATION NUMBER: 60/393,233
;  PRIOR FILING DATE: 2002-07-01
;  PRIOR APPLICATION NUMBER: 60/393,235
;  PRIOR FILING DATE: 2002-07-01
;  PRIOR APPLICATION NUMBER: 60/393,280
;  PRIOR FILING DATE: 2002-07-01
;  PRIOR APPLICATION NUMBER: 60/430,948
;  PRIOR FILING DATE: 2002-12-04
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 614
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 582
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-249-847-582

  Query Match             45.5%;  Score 45;  DB 7;  Length 487;
  Best Local Similarity   66.7%;  Pred. No. 27;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 SYDSIKLEPENP 12
              |:  ||| ||||
Db        233 SFSEIKLRPENP 244


RESULT 13
US-11-096-568A-28287
; Sequence 28287, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides E
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28287
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(361)
;   OTHER INFORMATION: Ceres Seq. ID no. 2711462
US-11-096-568A-28287

  Query Match             44.4%;  Score 44;  DB 7;  Length 361;
  Best Local Similarity   57.1%;  Pred. No. 27;
  Matches    8;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              |:|   | |||:||
Db        314 SVKATCEMPPPFEE 327


RESULT 14
US-11-096-568A-28286
; Sequence 28286, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28286
```

```
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(363)
;   OTHER INFORMATION: Ceres Seq. ID no. 2711461
US-11-096-568A-28286

  Query Match             44.4%;  Score 44;  DB 7;  Length 363;
  Best Local Similarity   57.1%;  Pred. No. 27;
  Matches    8;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              |:|    | |||:||
Db        316 SVKATCEMPPPFEE 329


RESULT 15
US-11-096-568A-28285
; Sequence 28285, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28285
;   LENGTH: 413
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(413)
;   OTHER INFORMATION: Ceres Seq. ID no. 2711460
US-11-096-568A-28285

  Query Match             44.4%;  Score 44;  DB 7;  Length 413;
  Best Local Similarity   57.1%;  Pred. No. 31;
  Matches    8;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              |:|    | |||:||
Db        366 SVKATCEMPPPFEE 379


Search completed: March 23, 2006, 16:53:27
Job time : 24 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 23, 2006, 16:48:43 ; Search time 47 Seconds
(without alignments)
31.663 Million cell updates/sec

Title: US-09-830-972A-2_COPY_623_640
Perfect score: 99
Sequence: 1 SYDSIKLEPENPPPYEEA 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	50.5	405	2	US-09-537-357-54	Sequence 54, Appl
2	46	46.5	475	1	US-08-484-200-2	Sequence 2, Appli
3	46	46.5	475	2	US-08-465-375-2	Sequence 2, Appli
4	46	46.5	475	2	US-08-764-870-10	Sequence 10, Appl
5	46	46.5	475	2	US-08-980-115-10	Sequence 10, Appl
6	46	46.5	475	2	US-09-788-070-2	Sequence 2, Appli
7	46	46.5	475	2	US-10-142-373-2	Sequence 2, Appli
8	46	46.5	475	2	US-09-587-549C-2	Sequence 2, Appli
9	46	46.5	475	2	US-09-155-252A-2	Sequence 2, Appli
10	46	46.5	476	2	US-08-134-557D-2	Sequence 2, Appli
11	46	46.5	477	2	US-09-128-142-2	Sequence 2, Appli
12	46	46.5	478	2	US-09-166-265-5	Sequence 5, Appli
13	46	46.5	478	2	US-09-765-111A-27	Sequence 27, Appl
14	46	46.5	505	2	US-09-128-142-4	Sequence 4, Appli
15	46	46.5	505	2	US-09-765-111A-16	Sequence 16, Appl
16	46	46.5	506	2	US-09-514-247A-6	Sequence 6, Appli
17	46	46.5	521	2	US-09-949-016-9620	Sequence 9620, Ap
18	46	46.5	521	2	US-09-949-016-9621	Sequence 9621, Ap
19	46	46.5	619	2	US-09-248-796A-20837	Sequence 20837, A
20	46	46.5	777	2	US-09-765-111A-2	Sequence 2, Appli
21	46	46.5	811	2	US-09-765-111A-23	Sequence 23, Appl
22	46	46.5	840	2	US-09-765-111A-4	Sequence 4, Appli
23	46	46.5	874	2	US-09-765-111A-6	Sequence 6, Appli
24	45	45.5	355	2	US-09-463-239-30	Sequence 30, Appl
25	45	45.5	529	2	US-09-489-039A-8824	Sequence 8824, Ap
26	44	44.4	247	2	US-09-248-796A-19810	Sequence 19810, A
27	44	44.4	250	1	US-08-861-269-5	Sequence 5, Appli
28	44	44.4	250	1	US-09-134-596-5	Sequence 5, Appli
29	44	44.4	250	2	US-09-293-273-5	Sequence 5, Appli
30	44	44.4	406	2	US-09-252-991A-32895	Sequence 32895, A
31	44	44.4	754	2	US-09-392-714-20	Sequence 20, Appl
32	44	44.4	800	2	US-09-538-092-1342	Sequence 1342, Ap
33	44	44.4	801	2	US-09-949-016-6588	Sequence 6588, Ap
34	44	44.4	810	2	US-09-949-016-11152	Sequence 11152, A
35	43	43.4	241	1	US-08-379-556A-4	Sequence 4, Appli
36	43	43.4	347	1	US-08-379-556A-2	Sequence 2, Appli
37	43	43.4	406	2	US-09-270-767-34561	Sequence 34561, A
38	43	43.4	406	2	US-09-270-767-49778	Sequence 49778, A
39	43	43.4	488	2	US-09-556-877-297	Sequence 297, App
40	43	43.4	488	2	US-09-620-412C-297	Sequence 297, App
41	43	43.4	488	2	US-09-598-419-297	Sequence 297, App
42	43	43.4	789	2	US-09-712-363-244	Sequence 244, App
43	43	43.4	912	2	US-08-943-768-2	Sequence 2, Appli
44	43	43.4	912	2	US-09-865-960-2	Sequence 2, Appli
45	43	43.4	928	2	US-09-336-946B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-537-357-54
; Sequence 54, Application US/09537357
; Patent No. 6271018
; GENERAL INFORMATION:
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE
; TITLE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.0002
; CURRENT APPLICATION NUMBER: US/09/537,357
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Guayule
US-09-537-357-54

Query Match 50.5%; Score 50; DB 2; Length 405;
Best Local Similarity 47.1%; Pred. No. 15;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 YDSIKLEPENPPPYEEA 18
              |:|:::||  || | :|
Db        180 YESLRIEPPVPPQYGKA 196
```

RESULT 2
US-08-484-200-2
; Sequence 2, Application US/08484200
; Patent No. 5861274
; GENERAL INFORMATION:
; APPLICANT: EVANS, RONALD M.
; APPLICANT: FORMAN, BARRY M.
; APPLICANT: KLIEWER, STEVEN A.
; APPLICANT: ONG, ESTELITA S.
; TITLE OF INVENTION: NOVEL MEMBERS OF THE STEROID/THYROID
; TITLE OF INVENTION: SUPERFAMILY AND USES THEREFOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 SOUTH FLOWER STREET, SUITE 2000
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,200
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  REITER, STEPHEN E.
;      REGISTRATION NUMBER:  31,192
;      REFERENCE/DOCKET NUMBER:  P41 9971
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-546-1995
;      TELEFAX:  619-546-9392
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  475 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-484-200-2

  Query Match             46.5%;  Score 46;  DB 1;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 70;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         75 AIKVEPASPPYYSE 88


RESULT 3
US-08-465-375-2
; Sequence 2, Application US/08465375A
; Patent No. 6022897
; GENERAL INFORMATION:
;  APPLICANT: Evans, Ronald M.
;  APPLICANT: Forman, Barry M.
;  TITLE OF INVENTION: SELECTIVE MODULATORS OF PEROXISOME
;  TITLE OF INVENTION: PROLIFERATOR ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE
;  TITLE OF INVENTION: USE THEREOF
;  FILE REFERENCE: SALK1470-1
;  CURRENT APPLICATION NUMBER: US/08/465,375A
;  CURRENT FILING DATE: 1995-06-05
;  EARLIER APPLICATION NUMBER: 08/428,559
;  EARLIER FILING DATE: 1995-04-25
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-08-465-375-2

  Query Match             46.5%;  Score 46;  DB 2;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 70;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         75 AIKVEPASPPYYSE 88


RESULT 4
US-08-764-870-10
; Sequence 10, Application US/08764870
; Patent No. 6236946
;  GENERAL INFORMATION:
;    APPLICANT:  Scanlan, Thomas S
;    APPLICANT:  Baxter, John D
;    APPLICANT:  Fletterick, Robert J
;    APPLICANT:  Wagner, Richard L
;    APPLICANT:  Kushner, Peter J
;    APPLICANT:  Apriletti, James W
;    APPLICANT:  West, Brian
;    TITLE OF INVENTION:  Nuclear Receptor Ligands and Ligand
;    TITLE OF INVENTION:  Binding Domains
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward
;      STREET:  Five Palo Alto Square,  3000 El Camino Real
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/764,870
;      FILING DATE:  13-DEC-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/008,540
;      FILING DATE:  13-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/008,543
;      FILING DATE:  13-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/008,606
;      FILING DATE:  14-DEC-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nakamura, Jackie N
;      REGISTRATION NUMBER:  35,966
;      REFERENCE/DOCKET NUMBER:  UCAL-246/01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)843-5000
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  475 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-764-870-10

  Query Match             46.5%;  Score 46;  DB 2;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 70;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         75 AIKVEPASPPYYSE 88


RESULT 5
US-08-980-115-10
; Sequence 10, Application US/08980115
; Patent No. 6266622
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Thomas S.
;  APPLICANT: Baxter, John D.
;  APPLICANT: Fletterick, Robert J.
;  APPLICANT: Wagner, Richard L.
;  APPLICANT: Kushner, Peter J.
;  APPLICANT: Apriletti, James W.
;  APPLICANT: West, Brian L.
;  APPLICANT: Shiau, Andrew K.
;  TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
;  FILE REFERENCE: UCAL-246/02US
;  CURRENT APPLICATION NUMBER: US/08/980,115
;  CURRENT FILING DATE: 1997-11-26
;  EARLIER APPLICATION NUMBER: 08/764,870
;  EARLIER FILING DATE: 1996-12-13
```

```
;  EARLIER APPLICATION NUMBER: 60/008,606
;  EARLIER FILING DATE: 1995-12-14
;  EARLIER APPLICATION NUMBER: 60/008,543
;  EARLIER FILING DATE: 1995-12-13
;  EARLIER APPLICATION NUMBER: 60/008,540
;  EARLIER FILING DATE: 1995-12-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (202)..(475)
;   OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-10

  Query Match             46.5%;  Score 46;  DB 2;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 70;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         75 AIKVEPASPPYYSE 88


RESULT 6
US-09-788-070-2
; Sequence 2, Application US/09788070
; Patent No. 6413994
; GENERAL INFORMATION:
;  APPLICANT: EVANS, Ronald
;  APPLICANT:  FORMAN, Barry
;  TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR-GAMMA,
;  TITLE OF INVENTION:  AND METHODS FOR THE USE THEREOF
;  FILE REFERENCE: SALK1480-2
;  CURRENT APPLICATION NUMBER: US/09/788,070
;  CURRENT FILING DATE:  2001-02-16
;  PRIOR APPLICATION NUMBER: US 09/955,302
;  PRIOR FILING DATE: 1999-02-22
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-09-788-070-2

  Query Match             46.5%;  Score 46;  DB 2;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 70;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         75 AIKVEPASPPYYSE 88


RESULT 7
US-10-142-373-2
; Sequence 2, Application US/10142373
; Patent No. 6605627
; GENERAL INFORMATION:
;  APPLICANT: EVANS, Ronald
;  APPLICANT:  FORMAN, Barry
;  TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED
;  TITLE OF INVENTION:  RECEPTOR-GAMMA,
;  TITLE OF INVENTION:  AND METHODS FOR THE USE THEREOF
;  FILE REFERENCE: SALK1480-2
;  CURRENT APPLICATION NUMBER: US/10/142,373
;  CURRENT FILING DATE:  2002-05-08
;  PRIOR APPLICATION NUMBER: US/09/788,070
;  PRIOR FILING DATE: 2001-02-16
;  PRIOR APPLICATION NUMBER: US 09/955,302
;  PRIOR FILING DATE: 1999-02-22
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-142-373-2

  Query Match             46.5%;  Score 46;  DB 2;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 70;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         75 AIKVEPASPPYYSE 88


RESULT 8
US-09-587-549C-2
; Sequence 2, Application US/09587549C
; Patent No. 6815168
; GENERAL INFORMATION:
;  APPLICANT: Greene, Marianne E.
;  APPLICANT:  Blumberg, Bruce E.
;  TITLE OF INVENTION: Human Peroxisome Proliferator Activated Receptor Gamma:
;  TITLE OF INVENTION:  Compositions and Methods
;  FILE REFERENCE: ARD
;  CURRENT APPLICATION NUMBER: US/09/587,549C
;  CURRENT FILING DATE:  2000-06-01
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-587-549C-2

  Query Match             46.5%;  Score 46;  DB 2;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 70;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         75 AIKVEPASPPYYSE 88


RESULT 9
US-09-155-252A-2
; Sequence 2, Application US/09155252A
; Patent No. 6830882
; GENERAL INFORMATION:
;  APPLICANT: EVANS, Ronald
;  APPLICANT:  FORMAN, Barry
;  TITLE OF INVENTION: SELECTIVE MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED
;  TITLE OF INVENTION:  RECEPTOR-GAMMA, AND METHODS FOR THE USE THEREOF
;  FILE REFERENCE: SALK1470-2
;  CURRENT APPLICATION NUMBER: US/09/155,252A
;  CURRENT FILING DATE:  1998-09-21
;  PRIOR APPLICATION NUMBER: PCT/US96/05465
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-09-155-252A-2

  Query Match             46.5%;  Score 46;  DB 2;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 70;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         75 AIKVEPASPPYYSE 88


RESULT 10
US-08-134-557D-2
; Sequence 2, Application US/08134557D
; Patent No. 6200802
;  GENERAL INFORMATION:
;    APPLICANT:  Greene, Marianne E.
;    APPLICANT:  Blumberg, Bruce
;    TITLE OF INVENTION:  Human Peroxisome Proliferator Activated
;    TITLE OF INVENTION:  Receptor Gamma:  Compositions and Methods
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rockey, Milnamow & Katz, Ltd.
;      STREET:  2 Prudential Plaza, Suite 4700 180 N. Stetson
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/134,557D
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Katz, Martin L.
;      REGISTRATION NUMBER:  25,011
;      REFERENCE/DOCKET NUMBER:  ARCH:098
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5400
;      TELEFAX:  312-616-5460
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  476 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-134-557D-2

  Query Match             46.5%;  Score 46;  DB 2;  Length 476;
  Best Local Similarity   57.1%;  Pred. No. 71;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         75 AIKVEPASPPYYSE 88


RESULT 11
US-09-128-142-2
; Sequence 2, Application US/09128142
; Patent No. 6294559
;   GENERAL INFORMATION:
;        APPLICANT: Smith, Roy G.
;        TITLE OF INVENTION: ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH
;                            PEROXISOME PROLIFERATOR ACTIVATED RECEPTORS GAMMA1 AND GAMM
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jack L. Tribble
;             STREET: 126 E. Lincoln Ave., P.O. Box 2000
;             CITY: Rahway
;             STATE: New Jersey
;             COUNTRY: US
;             ZIP: 07065-0907
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Power Macintosh 7500/100
;             SOFTWARE: Microsoft Word 6.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/128,142
;             FILING DATE: 03-Aug-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/844,007
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Tribble, Jack L.
;             REGISTRATION NUMBER: 32,633
;             REFERENCE/DOCKET NUMBER: <Unknown>
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (908) 594-5321
;             TELEFAX: (908) 594-4720
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 477 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-128-142-2

  Query Match             46.5%;  Score 46;  DB 2;  Length 477;
  Best Local Similarity   57.1%;  Pred. No. 71;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         77 AIKVEPASPPYYSE 90


RESULT 12
US-09-166-265-5
; Sequence 5, Application US/09166265
; Patent No. 6689574
; GENERAL INFORMATION:
;  APPLICANT: Cummings, Richard T.
;  APPLICANT: Hermes, Jeffrey D.
;  APPLICANT: Moller, David E.
;  APPLICANT: Zhou, Gaochao
;  TITLE OF INVENTION: ASSAYS FOR NUCLEAR RECEPTOR AGONISTS AND
;  TITLE OF INVENTION: ANTAGONISTS USING FLUORESCENCE RESONANCE ENERGY TRANSFER
;  FILE REFERENCE: 20017
;  CURRENT APPLICATION NUMBER: US/09/166,265
;  CURRENT FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 478
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-166-265-5

  Query Match             46.5%;  Score 46;  DB 2;  Length 478;
  Best Local Similarity   57.1%;  Pred. No. 71;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         77 AIKVEPASPPYYSE 90


RESULT 13
US-09-765-111A-27
; Sequence 27, Application US/09765111A
; Patent No. 6723506
; GENERAL INFORMATION:
```

```
;  APPLICANT: Fletcher, Jonathan A.
;  APPLICANT:  Kroll, Todd G.
;  TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
;  TITLE OF INVENTION:  AND POLYPEPTIDES AND USES THEREOF
;  FILE REFERENCE: B0801/7196/ERP/MAT
;  CURRENT APPLICATION NUMBER: US/09/765,111A
;  CURRENT FILING DATE:  2001-01-18
;  PRIOR APPLICATION NUMBER: US 60/177,109
;  PRIOR FILING DATE: 2000-01-20
;  PRIOR APPLICATION NUMBER: US 60/225,079
;  PRIOR FILING DATE: 2000-08-14
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
;   LENGTH: 478
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-765-111A-27

  Query Match             46.5%;  Score 46;  DB 2;  Length 478;
  Best Local Similarity   57.1%;  Pred. No. 71;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db         77 AIKVEPASPPYYSE 90


RESULT 14
US-09-128-142-4
; Sequence 4, Application US/09128142
; Patent No. 6294559
;   GENERAL INFORMATION:
;        APPLICANT: Smith, Roy G.
;        TITLE OF INVENTION: ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH
;                            PEROXISOME PROLIFERATOR ACTIVATED RECEPTORS GAMMA1 AND GAMM
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jack L. Tribble
;             STREET: 126 E. Lincoln Ave., P.O. Box 2000
;             CITY: Rahway
;             STATE: New Jersey
;             COUNTRY: US
;             ZIP: 07065-0907
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Power Macintosh 7500/100
;             SOFTWARE: Microsoft Word 6.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/128,142
;             FILING DATE: 03-Aug-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/844,007
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Tribble, Jack L.
;             REGISTRATION NUMBER: 32,633
;             REFERENCE/DOCKET NUMBER: <Unknown>
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (908) 594-5321
;             TELEFAX: (908) 594-4720
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 505 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-128-142-4

  Query Match             46.5%;  Score 46;  DB 2;  Length 505;
  Best Local Similarity   57.1%;  Pred. No. 75;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db        105 AIKVEPASPPYYSE 118


RESULT 15
US-09-765-111A-16
; Sequence 16, Application US/09765111A
; Patent No. 6723506
; GENERAL INFORMATION:
;  APPLICANT: Fletcher, Jonathan A.
;  APPLICANT:  Kroll, Todd G.
;  TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
;  TITLE OF INVENTION:  AND POLYPEPTIDES AND USES THEREOF
;  FILE REFERENCE: B0801/7196/ERP/MAT
;  CURRENT APPLICATION NUMBER: US/09/765,111A
;  CURRENT FILING DATE:  2001-01-18
;  PRIOR APPLICATION NUMBER: US 60/177,109
;  PRIOR FILING DATE: 2000-01-20
;  PRIOR APPLICATION NUMBER: US 60/225,079
;  PRIOR FILING DATE: 2000-08-14
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 505
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-765-111A-16

  Query Match             46.5%;  Score 46;  DB 2;  Length 505;
  Best Local Similarity   57.1%;  Pred. No. 75;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 SIKLEPENPPPYEE 17
              :||:|| :|| | |
Db        105 AIKVEPASPPYYSE 118


Search completed: March 23, 2006, 16:50:05
Job time : 47 secs
```